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AAW24121 standard; Protuli, 659 AA. AAW24121;

ALIGNMENTS

Procease; research resgire, thermal stability; thermococcus celer. 20-APR-1998 (first entry) Thermococcus protease.

Thermococcus celer DSM-1117. WO9721823-A1. 37*NOV-1996; 19-JUN-1997.

96WO-JPO ...

Assda K., Kato I., Mitta N., Morishita H., Takakura H., Tsunasawa S., Yamanoto K. (TAKI) TAKARA SHUZO CO 1275. 12-DEC-1995; 95JP-032: 10-

WPI; 1997-332794/30. N-PSDB; AAT85667.

Processe(s) and genes enrolling thes obtained from Thermococcus and Phrococcus strains - have extressly high thornal stability and ere used industrially and ex. research research research

W09856926-A1

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This sequence represents the protesse from Thermococcus caler DSH_2A/F6.
This sequence is a protesse of the invention. The protesses of Unit,
invention have extremely high thermal statility. The protesses on the Claim 1; Page 82-85; 159pp; Japanese chemical industries. **888888

659 Sequence

Caps 0: ö DB 18; Length 659; 0, Indels h Similarity 100.0%, Pred. No. 2.1e-203; 59; Conservative 0; Hismatches 0, Best Local Sim Matches 659; Query Match

61 DTVIMPGSYGDRDRAVKVLRLAGAQVKISYKIIPAVAVKIKARDLLLIAGHIDTGYFGNT 320 1 MKRIGAVYLALVLVGILAGTALAAPVKPVVRNNAVQQKNYGLLTPGLPKKVQRMWNOrv 60 1 NKRLGANVLALVLVGLLAGTALAAPVKPVTRNNAVQCKHTGLLTPGLFKKVCRNNNUGV 60 ò 쉺 ò

61 DTVIMEGSYGDRDRAVKVLRLMGAQVKYSFKIIDAVAVKIKARDLLLLAGANIDEGSFGNT 520 a

121 RVSGIKFIQEDTKVQVDDATSVSQIGADTVHNSLGYDGSGVVVAIVDTGIDANHPDLKGT 190 183 ò

VIGWYDAVHGRSTPYDDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGS 240'; 121 RVSCIRPIQEDYKVQVDDATSVSQLGADTVWNSLGTDGSGVVVAIVDTGIDANHPDLKGK 18 8 ò

181 VIGWYDAVHGRSTPYDDGGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGGGG 240 ...

241 VSTIIAGVDWVVQNKDKYGIRVINISLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNS 241 VSTILADVENVYCHKDKYGIRVIHLSLGSSOSSDGTDSLSGAVHÄMDAGIVVCVÄÄGHS a ò 8

GPNITYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASG 301

300 360

GPNTYTVGSPAASKYITVGAVDSNDNIASFSSSRGPTADGRLKPEVVAPGVDIIAPRASG 360 361 TSMGTPINDYYTKASGTSMATPHYSGYGALILQAHPSMTPDKVKTALIETADIVAPKEIA 420 161 TSMCTPINDYTTKASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIA 420 301 a Š a ò

481 DIYLYDPHGHEYDYSYTAYYGFEKYGYYNPTAGTWTVKYVSYKGAAHYQYDVYSDGSI.SQ 540

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LDLY LY DPNONLYDRST SSNSY EHY EYANPAPOTWTF LVY AY STYGWADYOLKAVVY TG* 659 541 SGGGNPNPNPNPNPTTDTGTFTGSVNDYNDTSDTFTMNVNSGATKITGDLTFDTS.ND 600-481 DENLYDPHGHEVDESYTATYGFERVGYYNPTAGTHTVK VVSYKGAANTQVDVVSDGS:3Q 540 541 SOCGNPNPNPNPNPTPTTDTGTFTGSVNDYWDTSDTFTMNVNSGATKITGDLFFDTSYND, 600 LDLYLYDPHGHLYDRSTSSHSYEHVEYANPAPGTWTPLYAYSTYGHADYQLAAVYYYG:659 601 8 ક 8 è

AAN94840 standard; Protein; 659 AAN94840; RESULT 2 AAW94840 ID AAW9

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(first entry) W09856926 Seq ID 12. 06-NAY-1999 FX8X83X8

Phermococcus celer

Hyperthermostable; protesse; thermophilic: bacterium; subtilisin additive; drug; vashing agent; foodstuff; chemical synthesis.

The uncomplication setters are a pyrethremeable process and efforted from a vertical properties of 10.0 Set (Ceptiman 10:54 Set), vertical policy of 20.0 Vertical verti Recombinant hyperthermostable protease from Pyrococcus furiosus . and gane encoding it, for large scale production of the protease for Shimojo T, Takakura Disclosure, Page 55-58, 82pp; Japanese. Asada K, Kato I, Morishita M, 98WO-JP024 S 97JP-0151969 (TAKI) TAKARA SHUZO CO WPI: 1999-080907/07 N-PSDB; AAX05926. Industrial use. 10-JUN-1997; 17-DEC-1998 25

1 WKRIGAVYLALVEVGILAGIALAAPVKPVYRNNAVQQKNYGLLTPGLFKKYQRHNWNQEV 60 Gapa ö ; Score 3437; DR 20: Length 659; ; Pred. No. 2.1e-203; 0; Mismatches 0; Indels 0; udery Match Best Local Stmilarity 100.0%; Matches 659; Conservative 0;

659 AA;

Seguence

9 1 MKRIGAVVIALVIVGILAGTALANDVKPVVRNNAVQGXNYGLLTPGLEKKVQRNNNNQGV ò ŏ

121 RVSGIKFIQEDYKVQVDDATSVSCIGADTVANSLGYDGSGVVVALVDTGIDANHPDIXGK a

121 RVSGIKFIQEDYKVQVD55GVSJIGADIYWNSLGYDGSGVVAIVDFGIDANHPDLKGK VIGWYDAVNGRSTPYDDDCM-H-AGIVAGTGSVNSQYIGVAPGAKLVGVKYLGADGSGS 181 음 ð

241 VSTIIAGVDWVVQNKDKY:IR":NLSLGSSQSSDGTDSLSQAVNNANDAGIVVCVAAGHS 300 2 8 ò 용 š

961 TSMGTPINDYYTKASGTSMITT TVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIA 420 용 გ ò

DIATGAGRVNVYKAIKTDD: AF :PFTGSVADKGSATHTFDVSGATFVTATLYMDTGSSDI 480 DIAYGAGRUNYYKAIXYDE# COPPEGSVADKGSAFHTFDVSGATFYTALLYMDTGSSDI (21

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AAW24123 standard: Protein; 659 AA.

RESULT 3

20-APR-1998 (first entry)

AAW24123; Protense.

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LGADGSGSVSTIIAGVDWYVQNKDXYGIRVINLSLGSSQSSDGTDSLSGAVNNAWDAGIV 292
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Tsunasava S. Yamamoto K.
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proceeded strains have extremely high thermal stability and are 
useful industrially and as research reasons.
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; Pred; No. 36-171;
47; Mismatches 46; Indels 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease: research reagent; thermal stability.
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96NO-JP03253.

W09721823-A1. 07 - NOV - 1996; 12-DEC-1995, 19-JUN-1997. Synthetic.

95JP-0323285.

Aaada K, Kato I, Mitta M, Tsunasova S, Yamamoto K,

(TAKI) TAKARA SHUZO CO LED WPI: 1997-332794/30. N-PSDB; AAT85669. Claim 9; Page 92-95; 159pp; Japanese.

8×888×8×111×8×8

Ouery Match Best Local Similarity 83.7%; Matches 558; Conservative 47

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659 AA;

Sequence

This sequence represents the protesse from Pyrococcus furiosus DSM-3638. Disclosure; Page 125-128, Jupp; Japanese.

174 HPDLKCKVIGHYDAVHGRSTPYDDGGHGTHVAGIVAGTGSV-NSQYIGVAPGAKLVGVKV 232

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293 VYVAAGHSGPHKYTIGSPAAASSVITYGAVDKYDVITSESSRGPIADGRAKPEVVANGEN 352
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193 THEFT FILLE F
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Best Local Similarity
                                                                                         Pyrococcus furiDaus
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB: AAX05929.
                                                                                                                                                                                                                                                          10-JUN-1997;
                                                                                                                               MOS855925-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                     59 EVDTVIMPGSTGDRORAVKYLRLHGAQVKYSYKIIPAVAVKTRARDLLLIAGMIDTGTFG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                             58 EISTVIYFRHEREXIAVRVLELMGARVRYVYHIIFALMADLXVRDLLVISGL--7G--6-113:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 KAKLSGVRFIQEDYKVTVSAKLEGIDESAAQVAATYVNN-LGTEGSGJTIGIIDTGTAS, 17,2
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                                                                                                                                                                                                                                                                                                                                                                           1 HKGLKALILVILVICLVVGSVAJAPERKVDOVRN --- VEKNYGLLIPGLFRKIOKLNPNE 57
                                                                                                                                                                                                                                                                                               96; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                     I NKRLGAVYLALVLVGLLAGTALAAPVKPV--VRNNAVQQXNYGLLTPGLFKKVQRNNANO 58
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                                                                                              This sequence is a protesse of the invention. The protesses of the invention have extremely high thermal stability. The protesses can threat as research respents, and industrially in the food, drug and otherwal industries.
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                                                                                                                                                                                                                                                Query Match 72.3%; Score 2483.5; DB 18; Length 554; Boat Local Similarity, 72.1%; Pred No. 8.9e.145; Matches 481, Conservative 59; Mismatches 96; Indels 21;
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Gaps

DB 20, Length 654; 96; Indels 21;

72.34: Score 2483.5: DB 20

59; Nismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinojo T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kato I, Morishita M.
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98WO-JP02465
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AAH24122;

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260 IRVINISLGSSQSSDGTDSL5GAVNNANDAGIVVCVAAGNSGPNTYTVGSPAAASKVITV 319
                                                                                                                                                                                      310 GAVDSNDNIASFSSRGPTACSFLKPEVVAPGVDIIAPRASGTSHGTPINDYYTKASGTSH 379
                                                                                                                                                                                                                                                                                           118 GAVDXXDZTSFSSRGPTADGRLXPEVVAPGNKIIAARASGTSMGOPINDYTAAPGTSM 247
                                                                                                                                                                                                                                                                                                                                                                       380 ATPHYSGVGALILQAHPSHTPDKVKTALIETADIVAPKEIADIAYGAGRVNYKAIKYDD 439
                                                                                                                                                                                                                                                                                                                                                                                                           YAKLTFTGSVADXGSATHTFDVSGATFVTATLYWDTGSSDIDLYLYDPNGNEVDYSYTAY 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 YGFEXVGYYNPIDGTWTIRVVSYSGSANYQVOVVSDGSLSQ....-PGSSPSPQPEPTVD 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 SANOVHATYVWN-LGYDGSC: TIGIIDIGIDASHPDLQGKVIGWDFVNGRSYPYDDHGH 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant hyperthermos above protease from Pyrococcus furiosus - or and game encoding It, for inge scale production of the protease for industrial use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hyperthermostable; protociae: thermophilic; bacterium: subtilisin; additive; drug; washing syent; foodstuff; chemical synthesis.
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                                   473 WDNANSDLDLYLYDPNGNQVDYSYTAYYGFEXVGYNHTDGTWTIKVVSYSGSANYQVDV $3:
           473 WDTGSSDIDLYLYDPNGNEVDYSYTAYYGFEKVGYYNPTAG7WTVXVVSYKGAANYQVDV: 433
                                                                                                                533 VSDGSLSQSGGGNPNPNPNPNPTTDTQTFTGSVNDYWDTSDTFTMNVNSGATKITGDL, 592
                                                                                                                                             533 VSGCSLSQ-----PGSSPSPGPEPTVDAKTFGGSDHYYTDRSDFFHTVNSGATKTTGDL 587
                                                                                                                                                                                                                          593 7PDTSTNDLDLYLYDPNGNLVDRS7SSNSYEHVEYANPADGTWFLYYAYSTYGMADYQL 652
                                                                                                                                                                                                                                                       188 VEDTS YNDLDLYLYDDWDXLVDRSES PNSYEHVEYLT PAPFOWYFLVYAYYTYGWAYYEL, 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 SVSQIGADTVANSLCYDGSGVVVAIVDTGIDANHPDLKGKVIGNYDAVNGRSTPYDDGG, 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protesse, research reagent; thermal stability; pyrococcus furicaus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Proceccus strains - have extremely high thermal stability and ave-
useful industrally and as research respants
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Tsunasawa S., Yamamoto K.
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Dest Local Similarity 78.3%; Pred. No. 1.1e-123;
Matches 407; Conservative 36; Mismatches 70;
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/note- "encoded by GNA"
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Misc-difference 428
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WPI: 1997-332794/30. N-PSDB; ANT85668.

12-DEC-1995;

W09721823-A1 19-JUN-1997. -3861-YOK-50

Query Metch Dest Local Similarity Seguence 522 AA;

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the question relates to a hyperparental process and derived fruit a version processes has occured that a continuous conti
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522 AA Sequence

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                                                                                                   141 SVSQIGADTVHNSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRSTPYDDQGH 200
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Query Match 62.21, Score 2138.5; DB 20: Length 522; "
Seat Local Similarity 78, Page No. 1.5-1.21; Matches 407; Conservative 36; Mismatches 70: Indes 7; Gaps
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AAW94836 standard; Protein; 412

NSYEHVEYANPAPGTWTFLVYAYSTYGWADYQLKAVVYYG 659

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Hyperthermostable; protease; thermophilic; bacterium; subtilisin; additive; drug; washing agent; foodstuff; chemical synthesis. Hyperthermostable protease fragment 06-MAY-1999 (first entry) AAM94836;

Pyrococcus furiosus. W09856926-A1.

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the avenue or letter and aventuencenthe process derived from a vortise presentation by the control of the contr
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N-PSDB; AAK05920.
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141 SVSQIGADTVANSLGYDGSGYV/A(VDTGIDANHPDLKGKVIGHYDAVNGRSTPYDDQGH 200
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                     Length 412:
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illarity 80.64; Pred. No. 2.9e-97;
Conservative 129; Mixmarthhe
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Matches 325;
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AAR87009

Ź AAR87009 standard; Protein; 237 AAR87009;

MO9534645-A1 26-JUL-1994; 13-JUN-1994; 35-3UN-1995. 21-DEC-1995

fanamoto X;

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200 HGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKYLGADGSGSVSTIIAGVDARVQNKDKYG 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Invention relates to 4 year (AA708141) that codes for a hyperthemostable process: (AA87007) of Pyrococcus furlosus. 2 DN sequences (AA708133-34) are provided encoding paptides (AA87010-11).
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                     Protease; hyperthermostable; thermostability
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94JP-0136236.
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                                                                Pyrococcus furiosus.
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13-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AGUSGPHTYTVGSPAAASKVITVGAVDSHDAIASFSSGGPTAOGREKPEVVAPGVDIIA, 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DLKGKVIGHYDAVNGRSTPTDDGGGGTHVAGIVAGTGSVHSQYIGVAPGAKLGVGKVLGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.6%; Score 1154; DB 17; Length 237; 97.4%; Pred. No. 1.5e-63; Live 1; Mismatches 5; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus furlosus hyper:thermostable protesse gene - useful for recombinant prodm. of hyper:thermostable protesse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Investion relates to the hypotrhermostable protease of 
Pyropocrase fuctosus and it produ. as a secondamic procein 
the transforance using no vector carrying the processe geae 
(AVYGB111, A general on the vector carrying the processe general 
AVYGB111 and its encoded procein in AMSB1012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 PRASGTSWGTPINDYYTKASGTSMATPHVSGVGALILQAMPSHTPDKVKT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRASCTSMGTPINDTXNKQSGSSMCTPHVSGVGGLILQAHPSMTPDKVKT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morishita M, Tsunasawa S;
                                                                                                                                                                                                                                                /note= "unspecified amino acid"
                                                                                                Protease, hyperthermostable, thermostability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3: Page 70-71; 85pp; Japanese.
                                                                                                                                                                                     har-difference 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AARB7011 standard; Peptide; 188
                                                                                                                                                                                                                                                                                                                                                                                                95WO-JP01095.
                                                                                                                                                                                                                                                                                                                                                                                                                                           94JP-0173912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Asada K, Kato I, Mitta M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKARA SHUZO CO LITD.
                                                     Hyperthermostable protease.
10-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 97.4%
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-1996 (first entry)
                                                                                                                                                Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-049674/05.
N-PSDB; AAT08131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 237 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide sequence
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AAR87011; AAR87011

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This sequence is an asymptotic bindings accorded to Streptocyces this experience in the streptocyce this experience acts on f-shelltited-1.4 childropyclopic acts on f-shelltited-1.4 childropyclopic of 4-shelltited-1.4 chindropyclotic sector of shirs peritally applicated to the control of 4-shelltited-1.4 chindropyclotic sectors to online peritally applicated-1.4 chindropyclotic sectors to online peritally settled of 4-shelltited-1.4 chindropyclotic sectors to online peritally settled of 4-shelltited-1.4 chindropyclotic sectors of 6-shelltited-1.4 chindropyclotic sectors of 6-shelltited-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555 GFFILGATTVTVPA---G-SASYDMFADTRLGGTVDGAYSAYVVATGGGQTVRTAAAVQR 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....NVNSGATKITGDLFFDT-STNDLDLYLYDPNGNLV 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 VSQIGADTVWNSLGYDGSGVVVR.VDTGIDANHPDLKGKVIGHYDAVNGRSTP--YDDQG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 HGTHVAGIVAGTGSVN-SQYJGVAPGAKLVGVKVLGADGSGSVSTIIAGVDW7VQNKDKY 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 HGTHVASIAAGTGAQSKGKY:3VAPGAAILAGKVLDDSGPGDDSGILAGHEWAAQ---- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 CIRVINLSLGSSQSSDGTDSLSQAVNN-AMDAGIVYCVAAGNSGPNTTVGSPAAASKVI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GADVVNMSLGGMDTPE-TDPIEAAVDKLSAEKGVLFAIAAGNEGPE--SIGSPCSADAAL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 TVGAVDSNDNIASPSSRGP-TADSRLKPEVVAPGVDITAPRASGTSMGTPIND---YYTK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 TVGAVDDKDKLADPSSTGPRLGEGAIKPDVTAPGVDITAASABGNDIGGEVGEGPAGTMT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASGISMAIPHVSGVGALILQÄHPSWIPDKVKTALIETADIVAPKEIADIAYGAGRVNYK 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 ISGTSWATPHVAGAAALLKQQBPTWTSAELKGAL--TGSTKGGK-TTPFEQGSGRIQADK 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 LPADAARLVASGKIDRRLPDITELG--KAATRNSQKQGLKVIV---GYQGAARAAKAEVR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 LAAPVKPVVRNNAVQQKNYG;.L@PGLFKKVQRMNHNQEVDTVIHFGSYGDRDRAVKVLRL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YDDYAKLTFTGSVADKGSATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612 EVESYDVIVERIGEDGEPT PRETIDITION AGEGSGROYG-----AVAIDITALIELP
                                                                                                                                                                                                                                                                                                                                                                                                                                           Asymmetric hydrolase gens derived from streptomyees viridosporus -
acts on 4-substituted-1,4-1, hydropyidine derivatives to produce
Phitel derivatives useful for synthesis of cardiovascular drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 MGAQVKYSYKIIPAVAVKIKARFILLIAGMIDTGYFGNTRVSGIKFIQEDYKVQVDDATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 EAGELRRILITSLNADAVRTPHT: ---ASELWDAVTNODRIASGIAHVWLDGVRRAALDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 734;
                                                                                                                                                                                                        Matsufuji H, Nakashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 665; DB 18; 1
pred. No. 7,1e-33;
34; Hismatches 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 49-55; 78pp: Japanese
                                                                                                                                                                                       zpshiki K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.24
        95JP-0212975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 31.24
Matches 216; Conservative
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                                                                                                                                                                                                        Arisava A, Dobashi K,
Tsuruta T, Yoshioka T;
                                                                                                                          (SAOC ) MERCIAN CORP.
                                                                                                                                                                                                                                                                                                                          WPI: 1997-145682/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                734 AA;
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT61454.
29-FEB-1996;
31-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White sequence represents a fragement of the protess (for Phermococous, color INSW-276 (see AMSQ121 for full length sequence). This sequence is a fragement of the protesses of the invention. The processes of the invention. The processes of the invention have extremely high themsal stability. The processes of the invention have extremely high themsal stability. The processes on be observed in the processes of the invention of the processes of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 HGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVXVLGADGSGSVSTTIAGVDAYVQNKDKYG 255°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 IRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVCVAAGNSGPNTYTVGSPAAASKVITV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 GAVDSHDNIASFSSEGPTADGRLKPEVVAPGVDIJAPRASG7SMG1PINDYYTKASGTSM 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 GAVDSNDMIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDYTKASGTSM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 IRVINISLGSSQSSDGADSLSQAVNNAWDAGIVYCVAAGNSGPWYYTVGSPAAASKVITV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 HGTHVAGTVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKYG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asymmetric hydrolass; dhpA; 4-substituted-1.4-dihydropyridine;
dediyyative; Stepponpores Viiloboporus; ester; dhrah; synthesi;
cardiyyative; Stepponpores Viiloboporus; aschemic heart disease;
cardiyative; steatment; hyper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cocation/Qualiflers
205..724
/note- "fragment of dhpA protein; see ANN13666"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protease(s) and genes encoding them obtained from thermococcus pyrococcus strains. There extremely high thermal stability and useful industrially and as research reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 188:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                 Morishita M. Takakura H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 27.3%; Score 935; DB 18; al Similarity 98.4%; Pred. No. 3.3e-50; 184; Conservative 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces viridosporus dhpA gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 110-112; 159pp; Japanese
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                                                                                                                                                                                                                                   Kato I, Mitta M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95WO-JP02147
                                                             95JP-0323285.
                                                                                                                                           (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36-OCT-1997 (first entry)
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                                                                                                                                                                                                                                                                     Tsunasawa S, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                    NPI; 1997-332794/30.
N-PSDB: AAT85676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 ATPHVTG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 ATPHYSG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09705243-A1
                                                                     12-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-1997.
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82 MGAQVKYSYKIIPAVAVKIFARDLLLIAGNIDTGYFGNTRVSGIKFIQEDYKVQVDDATS 141
                                                                                             152 EAGELRRTLTSLNADAVRTPHED---ASELWDAVINGERRASGIAHVWI.DGVRRAALDTS 208
                                                                                                                                                                142 VSDIGADTVANSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGHYDAVNCRSTP--YDDQG 199
                                                                                                                                                                                                        209 VQDIGAPKAN-SACTDCKQVXIAVLDTQVDTSHPLLKGRVTA---SKNFTAAPGAGDKVG 264
                                                                                                                                                                                                                                                                                  200 HGTHYAGIVAGTGSVN-SQYLGVAPGAKLVGVXVLGADGSGSVSTLIAGVDHVVQHKDKY 258
                                                                                                                                                                                                                                                                                                                                       265 HGTHVASIAAGTGAGSKGKYKGVAPGAALLNGKYLDDSGPGDDSGILAGNENAAAG---- 320
                                                                                                                                                                                                                                                                                                                                                                                                   159 GIRVINLSLGSSQSSDGTDSLSQAVNN-AMDAGTVVCVAAGNSGAWTYTVGSPAAASKVI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                  318 TVGAVDSNDNIASFSSKG2-PADGREKPEVVAPGVDIIAPRASGTSKGTPIND---TYTX 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 ASCISNATPHYSGYGALLIQAHISNTPDKVKTALIETADLYAPKEIADIAYGAGRYWYX 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 AIK----YDDYAKL/PPIGSVADKGSATH 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495 ALCOTVIADPVSVSFGVQ;WPHTDDEPVTXQLTYRNLGTQDVTLKLTSTATDPXGKAAPA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 TPDVSGATEVTATLYMDTGGSDIDLYLIDPNGNEVDYSYTAYYGPEXVGYYNPTAGTWTV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 GERTLGATIVIVPA --- GG: ASVDWTADTRLGGTVDGATSAYVVATGGGGTVRTAAAVOR 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  564 TGS-VHDYMD7SD7PTN------NVNSGATXI7GDL7ED7-SYNDLDLYLYDPNGNLV 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       663 KGTYLVDSWIAKDFGTLKGGTOMLVOPKLSVTXDT-TLTLDARTTXAADITVPDDK---- 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIB XVVSY-----XGF-UKKNYDVVSDGSLSOSGGGNPNPNPNPNPNPNPTPTTDTGTF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      612 EVESYDVTVRHIGROGKPTSERLTDLIGYAGLGSGROYG-----APATDTATLRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      derywetric hydrolase; dhpA/ 4-substituted-1,4-dihydropytidine;
derywetive; Strebowyses "teledapozus, seter; chiral; synthasis;
cardiowsesiar; treatment; hypertession; sechsenic heart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- 'ser232 as indicated in the apecification'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         718 ------AxPLSA: -IGYTYDTAG 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location '?ual' flera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO9705243-AL
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31.2%; Pred. No. 8.2e-33;
Live. 84; Hismatches 269; Indels 124; Gaps: 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in Geologica, is distant percent companying the companying at the companying of the companying at the 
663 KGTYLVDSWIAKDPGTLXGGIDMLVQPKLSVTXDT-TLTLDARTIKAADITVPDPK---- 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              esymmetric hidrolaes; dhoà: 4-subetituted-1.4-dihydropyridine.
1-dihydile: Streptopyces Viildoppores; ester: chital; synthesis:
cardiovescular; trosimon; hipertunsion; seobastic heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arisawa A, Dobashi K. Isshiki K, Mataufuji M, Nakashima T;
Tsuruta T, Yoshibka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "melanin (partial sequence).
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205..724
/note - see AAN13666 •
                                                            614 DRSTSSNSYEHVETANPARGTWIFLVYAYSTYG 646
                                                                                                                        AKPLSAT -- IGYTYDTAG 733
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                                                                                                                                                                                                                                                                    AAW13668 standard: Protein: 823 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Streptomyces viridosporus.
Chimeric Streptomyces antibioticus.
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Best Local Similarity 31,24
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAOC ) MERCIAN CORP.
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N-PSDB; AAT61455.
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31-JUL-1995;
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29-FEB-1996; 31-JUL-1995;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 VVCVAAGNSGPHIYTVGSPARASKVITVGAVDSNDNIASFSSRGP-TADGRLXPEVVAPG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 DLKGKUTGHYDAVNCRSTPX- : TAGGHGTHVAGIVAGTGSVN-SQYIGVAPGAKLVGVKV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 DIKGOVTA---SKNFTSAPTTV--VGHOTHVASIAAGTGAGSKGTYKGVAPGAKILNGKY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 LDDAGTGDDSGTLAGHENAAAQ----GADIVNASIGGHDTPE-TDPLEAAVDKLSARKGI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 GHTRVSGIKE108D--YKVQVWAATSVSGIGADTVMNSLGYDGSGVVVAIVDTGIDANHP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 GDRTASGVARVALDGVRKASL)--TSVGQIGTPRAMRA-GYDGRGVKIAVLDTGVDATHP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Efficient secretory production of foreign proteins e.g. traply transglutaminase employing transformant corynetors bacterium, steply industrial scale with direct concern for use in food processing and industrial scale with direct concern for use in food processing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18:5N: Score 636; DB 22; Length 1079; Bost Local Similarity 32.74 Fred: No. 6:96-31; Indels 132; Matches 201; Conservative 1; Mighatches 239; Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yokoyama K, Matsui H;
                                                                                                                                                                      Corynoform Dacterla: transglutaminase; food processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 113-120; 151np; Japanese.
                                                                                                                 38
                                                                                                                 Transglutaminase related probein SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unesava Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1999; 99up-0280098.
28-JUN-2000; 2000JP-0194043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-SEP-2000; 2000MQ-JP06780.
                                                                                                                                                                                                                                                         Streptomyces albogriseolus
                                                            13-JUL-2001 (first ontry)
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sorts on 4-asbetituetel-1,4-distryctoyridine derivetives to produce
histal derivetives usasiul for synthesis of cardiovascular drugs
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                                                                                                                                                                                                           Isshiki K.
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Matches 179; Conservative
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Tsuruta T, Yoshioka T:
                                                                                                                                               (SACC ) MERCIAN CORP.
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491 BUDYSYTAYYGFEKYGYINPTAGTHTVXVYSY 529 553 ADDCTESATVATGAGGSVETAAAVEREVESTAVTLAVLDRSGRATANVAATLSGLTGLT 612 560 TO-----TETGSVNOVMOTSDTFTMNVNSGATKITGDLTFDTSKNDLDLYLYDPMGNL 612 673 ARRAKPYKYTVPGKAAKAGFASADYTIETNDSAVSYGWALENYSGFRSAHL-----GPQ 726 Search completed: October 31, 2002, 13:29:40 Job time : 34 secs 613 YDRSTSSNSYEHVEYANPAPGTWT 636 727 ITHGTLSOQW-NTHESHGAKAOYT 749

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Copytight GenCoro werlinn 5.1.3 ON PROCRAM - POTATION SETTING 19.1931 - 1002 Compages Ltd. ON PROCRAM - POTATION SETTING SETTING SETTING Ltd. Ann On October 31, 2002, 13.1981 - SERTING Lines at 19.8000000 Filtis: 105-09-1-153-1 Filtis: 105-0	Minimum DB seq longth; Order parameters: 231628 Maximum DB seq longth; Order parameters: 231628	POST-PROCESSARION FALSIAN MANAGEMENT OF THE AMERICAN PARTIES AND AMERICA	Proc. in the measure of county prefetcing the chance there a confer system of the confer of the conf	11 10 10 10 10 10 10 10

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                                                 Quary Watch
100.08; Score 3437; DB 4;
Beat focal Stallarity 100.08; Pred. No. 6.7e-237;
Natches 659; Conservative U. Hismatches 0;
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419 Seventh Stree: N.M., Ste. 300
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Patent No. 6261822
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MORISHITA, Mic
YAMAMOTO, Katriüh: ko
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TITI: OP INVENTION: H:
NUMBER OF SEQUENCES: "4
CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APALICANT MONESTATA, MIO
APALICANT MONESTATA, MIO
APALICANT SERVICO, TORNICO
TELES TORNICOS, STEER TOR INTERPESSION OFFENDATION OFFENDATION OF THE BESSERE TAXABLE TO THE APACIFACTOR OFFENDATION OFFE
                                                                                                            100.0%; Scorm 3437; DB 4; Langth 659;
100.0%; Pred. No. 6.7e-237; Indels 0;
Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 151969/1997
PRIOR FILING DATE: 1997-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-445-472-12
; Squence 12, Application US/09445472
; Patent No. 6358726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin version 3,0
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SOFTWARE: Patentin versio
SEQ ID NO 12
                                                                                                                                                                                                     Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: TAKAKURA,
                                                                               US-08-894-818B-1
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59 EVDTVIMEGSYGDRDRAVTVLRLHGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTGYFG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HKRLGAVVLALVLUGLLAGTALAAPVKPV--VRNNAVOOKHYGLLTPGLFYKVORNNHNG 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KATD, IXUNDAHIN
THILE OF KRUNTION: HYPERTHERMOSTABLE PROTEASE GENES
WINGER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODIVATER: INP CONDACTURE
CORPLANTS: STR PC CONDACTURE
CORPLANTS SYSTEM: PC COSS/AS-DOS
CORRENT PRELICATION DAY-BORD
CORRENT PRELICATION NUMBER: 3-698-94-8188
FILLIAN DAYER: 3-498-94-8188
FILLIAN DAYER: 3-498-94-8188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSER: Browdy and Nelmark
STREET: 419 Seventh Street N.H., Ste. 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Weshington
STATE: D.C.
COUNTR: United States of America
21P: 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application US/088948188 Pacent No. 6251822 GENERAL INFORMATION: APPLICANT: TAKAKURA, HIGH APPLICANT: WORISHITA, MIGHAM APPLICANT: WANAWOTO, KCTSHIKO APPLICANT: YAWAWOTO, KCTSHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MITTA, Masshori
APPLICANT: ASADA, KIYOZO
APPLICANT: TSUNASAWA, SYSUMU
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-52:99
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APPLICATION WURBER: PT.7JBF
FILING DAYS: 07-00-1995
PRIOR APPLICATION DAYA: 1935
APPLICATION WORBER: 32-325
FILING DAYE: 12-3DG-7395
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ENFORMATION FOR SEC ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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US-08-894-8188-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM
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653 KAVVYYG 659
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233 GAROSGESTEITAGYDHYVORRDKTGIRVINLSLOSSOSSOGTOSLSOAVNAMDAGIY 392
233 GAROSGESTEITAGYBHYDDRGRKTGIRVINLSLOSSOSSOGTOSLSOAVNAMDAGIY 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 WDTGSSDIDLY LY DPNGNEVDYSYTAYYGFEKVGYYNPTAGTWTVKVVSYKGAANYQVDV: 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 IVAPKEIADIAYGAGRVHVYKAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFV7ATLY 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HERICAUVILALVINGILAGTALAAPVKPV - VRNNANGOKNYGLLTPGLERKVQRMMNQ '58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKGLKALILVILVIGLVVGSVAAAPEKKVEQVRN---VEKNYGLLTPGLFRKIQKLNFNE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Indels 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.8%; Score 2914; DB 4; Length 659;
83.7%; Pred. No. 1.1e-199;
11ve 47; Niematches 46; Indels 16
MEDIUM TYPE: "Pippy disk
CCHPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETEATIN RELease #1.0, Version #1.30
CURRENT APPLICATION DAYN:
                                                                                                                                                                            APPLICATION NUMBER: US/08/894,818B
FILING DATE: 20-MAY-1998
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TELECOMMINICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-328
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 659 amino acids
TYPE: amino acid
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LENGTH: 659 anino sold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Browdy, Roger L.
REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                           FILING DATE: 20
CLASSIFICATION:
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473 WOTGSSDIOLYLYDPHGNEVDYSYTAYYGPEKVGYYNPTAGTHTVKVVSYKGAANYQVDV 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 TPDISYNDLDLYLYDPNGELVDRETSSNSYBHVEYANPAPGTWTPLYYAYSTYGWADYOL 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              588 VFDTSYHDLDLYLYDPNDKLVDREBSPNSYEHVEYLJTPAPCTHYFLVYATYITGMAXYEL 647
                                                                                      119 WIRVSGIKFIQEDYKVQVDDA ----TSVSQIGADIVWNSLGYDGSGVVVALVDIGIDAN 173
                                                                                                                  114 KAKLSGVRFIGEDFXVIVSARLESLDESAAQVMATVUN-LGYDSSGITIGILDFGIDAG 172
                                                                                                                                                                                                        LGADGSGSVSTITAGVDWVVQUKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGIV 292
                                                                                                                                                                                                                                                                                                        233 LGADGSGSISTIIKGVEMAVDAKDKYGIKVINLSLGSSGSSGGTDALSDAVNAAWDAGLV 292
                                                                                                                                                                                                                                                                                                                                                   293 VCVAAGNSGPNTYTVGSPAAASKYITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                                                                                                                                                                                                                                                                                                                           193 VVVAAGNSGPIKKTIGSPAAASKVITVGAVDKTDVITSESSRGPTADGRIKPEVVARGGN 352
                                                                                                                                                                                                                                                                                                                                                                                                                                    353 LIAPRASCTSMCTPINDYYTKASCTSMATPHVSGVGALILQAHPSNTPDKVKTALIETAD 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 IVAPKEIADTAYGAGRVNVYKAIKYDDYAKLTPTGSVADKGSATHTFDYSGATFVTATLY 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVDTVINFGSYGDRDRAVKVI.RLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTGYFG 118
                       174 HPDLKGKVIGHYDAVNGRSTP103QGHGTHVAGIVAGTGSV-NSOYIGVAPGAKLVGVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HYPEYTHERMOSTABLE PROTEASE GENES HIMBER OF SEQUENCES: 42
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E: Browdy and Mainark
419 Seventh Streat N.W., Ste. 300
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Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDICANT MOTERATOR HILFT
APPLICANT MOTERATOR ASTOLICANT
APPLICANT VANDOZIO MSTUDILO
APPLICANT SADA. KLYOZ.
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                                                                                                                                                                                                                                                                           233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    473 MCTGSSDIDLYLYDPNGNEVDYSTAYTGPEKVGYYNPTAGIWTVKVVSYKGAANYQVDV 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 VSECSLSOSGGGNPNPNPNPNPNPTPTTTGTFTGSVNDYMDTSDTFTMNVNSGATKITGDL 592.
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                                                    114 KAKLSGVRFIGEDYKVTVSAELEGLESSAAQVMATYVWN-LGYDGSGITIGIIDTGIDAS 172
                                                                                                    174 HPDLKGKVIGWYDAVHGRSTPYDDQGHGTHVAGIVAGTGSV-NSQYIGVAPGAKLVGVKV 2\$2
                                                                                                                            1173 HPDLQGKVIGWVDFVWGKSYPYDDGGGTHVASIAAGTGAASNGXYKGMAFGAKLAGIKV 222
                                                                                                                                                                                          233 LGADGSGSVSTIIAGYDWYVONKDKYGIRVINLSLGSSOSSDGTDSLSOAVNNAWDAGIV 292
                                                                                                                                                                                                                       293 VCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                                                                                                                                                                                                                                                   293 VVVAAGNSGPIKYTIGSPAASKVITVGAVOKTOVITSESSRGPTADGREKPEVVAPGINF 352
                                                                                                                                                                                                                                                                                                                                                                 353 ILAPRASCISMOTPINDYTXASCISMATPHVSGVGALLLQANPSHTPDKVKTALIETAD 412
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.11; score 248.5; nm 4: Length 654; sest Local Similarity 77.11; pre-64 No. 5:10-159; Managers 481; Conservative 69; Mismacches 95; Indels 21; Gaps
         119 NPRYSGIKFIQEDYKVQVDDA-----TSVSQIGADTVWNSLGYDGSGVVVAIVDTGIDAA<sup>*</sup>173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ASADA, KLYOZO
APPLICANT: KATO, XLUNGASIA
1711& OF INVENTION: SYSTEM FOR EXPRPESSING HYPERTHERWOSTABLE
PILD REFERENCE: TAKAKURA-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/445,472
CURRENT FILING DATE: 1999-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 11969/1997
PRIOR FILING DATE: 1997-06-10
NUMBER OF SED ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09445472
Patent No. 6358726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin version 3.0
SEQ ID NO 16
LENGTH: 654
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APPLICANT: MORISHITA, MIO
APPLICANT: SHIMOJO, TOMOKO
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COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-D)://MS-DOS
SOFTWARE: Pc-DI://MS-DOS
SOFTWARE: Pc-tentin Wel-ess #1.0, Wersion #1.30
CURRENT APPLICATION DATA

1 MKRLGAVVLALVIJELAGTALAAPVKPV - VRNAVQOKNYGLLT PGLPKKVQRANNNO 58 1 HIGH THE STATE OF THE STATE O

TYPE: PRT

Floppy disk

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440 YAKLTFTGSVADKGSATHTFDVSGATPVTATLYWDTGSSDIDLYLYDPWGNEVDYSVTAY 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.2%; Score 2138.5; DB 4; Length 522;
78.3%; Pred. No. 1.4e-144;
tive 36; Mismatches 70; Indels 7; Gape
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                                                                                                    PROOF APPLICATION DAYS 1999
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                                     US/08/894,818B
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; Sequence 4, Application US/09445472
; Patent No. 638926
; GENERAL INFORMATION:
APPLICATION NUMBER: US/08
FILING DATE: 20-MAY-1998
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Best Local Similarity 78.38
Matches 407: Conservative
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MOLECULE TYPE: peptide
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141 SYSQIGADTVWHSLGYDGSG*YVAIVDTGIDANHPDLKGXVIG#YDAVNGRSTPYDDDGH 200
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68 GTHYASIAAGTGAASKGTKTAAGAAKLGIKVGAGGSSSSISTIIGVBAAVQHKBYG 127
68 GTHYASIAAGTGAASKGTKTAAGAAKLGIKVGAGGSSISTIIGVBAAVQHKBY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ocery Messer (2.37), Score 2138.5; DB 4; Length 522; Pered No. 14e-144; Pered No. 14e-144; Metches 407; Conservative 55; Misserchos 70; Indexs 7;
                  APPLICATE CONSULTY, MINA
APPLICATE SIRRON, TREES
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LOCATION: (428)
COMES TON: (428)
US-09-4445-472-4
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Premise 10 59978
Application Tokkoba, Hibaru
Application Tokkoba, Tokkoba
Application SERMON, Tokkob
APPLICATION SERMON, NIOSE
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TAKAKURA, HIKS JU
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61 DGSGSYSTITAGYDMYORNEDKYCLWYINLSIGSSGGSBGTDSLSGAVNRAMBAGIAVCY 120
61 DGSGSYSTITAGYDMYORNEDKTRYINLSIGSSGSBGTDSLSGAVNRAMBAGIAVCY 120
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121 AAGNSGPKTTVGSPAAASKVIIVGAVDSKDKIASFSSRGPTADGKIAPEVVARGVDIIA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 DLKGKVIGWDAVNGRSTPYDISGRHOTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGA 235
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                                                                                                                                                                RESULT 10
US-09-000-016-4
Sequence 4, Application US/0900f016
patent No. 6143541
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ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
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US-08-750-532-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 IRVINISLOSSOSSOGTOSLSOAVNANDAGIVYCVAAGNSOPNIYTVGSPAASKVITV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 INVINISEGSSOSSOSTBALSGAVANANBAGEVVVVAAGNSOPAKTEGSPBAASKUTV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 49.7%, Score 1707; DB 4; Langth 412; Spat Local Statlarity 80.6%; Pred: No. 5.1e-114; Index 2; Gapa Witches 315; Conservative 79; Mismatches 47; Index 2; Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 SVSQIGADTVKNSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGWYDAVNGRSTPYDDGGT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 SAAQWARTYWN - LOYDGSGITLGIIDTGIDASHPDLQGAVIGHVDBWGRSPYDBWGH'67
                                                                AMERICAN TROO, IMPORTANT AND AMERICAN DEPORTS ON PRETIDENCES AND THE OFFICE AMERICAN AMERICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE STATE OF THE S
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419 Seventh Street N.W., Sulte 300
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Patent No. 5756339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pyrococcus furiosus
US-09-445-472-1
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MEDIUM TYPE: FLOPPY
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 LPADAARLVASGKLDRRLFEDITELG -- KAATRNSGKGGLKVIV--- GYGGAARAAKAEVR 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 GADVVNMSLGGMDTPE-TD: EAVOKLSAEKGVLFAIAAGNEGPE--SIGSPGSADAAL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 LAAPVKPVVRNHAVQQKHYCLI, PPGLEKKYQRHNWNQEVDTVIMFGSYGDRDRAVKVLRL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Annual System - Annual System 
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MEDIUM TYPE: DISACETE: 3.5 Inch. 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-008
                                                             -----AKPLS47---IGYTYDTAG 733
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FILING DATE: Annuary 30, 1998
EASSPECTOR DATE: 30
PRLICATION DATE:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATIOS:
                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/99000016
Patent No. 6143541
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RECISEATION NUMBER: 73367
RECOMMENTATION HUMBER: TELECOMMUNICATION HUMBER: TELECOMMUNICATION HUMBER: 202-721-8240
TELERAX: 202-721-8240
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LENTH: 823 amino acida
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linesr
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US-09-000-016-2
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US-09-000-016-2
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Best Local Similarity 31.31, Soore 665, DB 4; Length 734,
Matches 216; Conservaties 84; Mismiches 289; Indels 124; Gaps
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209 VGGIGAPKAH-SATOGGGVRALVDTGOTSBDLAGRATA--SKIPTAAPGADGW3.323
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APLICATION WEBSITE, 155,047000 0.5
FILED DATE: JABLARY 10,1389
PROD. REPLECTION NAME TO APLICATION NAME TO APLICATION NAME TO APLICATION NAMES: JABLARY 10,100 NAMES TO APLICATION NAMES T
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SEQUENCE CLARACTERISTICS.
LENTH: 714 mino acide
TYPE: mino acide
STAMORDERS: might
TODOLOGY: linear
NOBLETTYPE: procein
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232 HTISGTSNATPHVAGAAALLKQQHPDWTSAELKGAL--TGSTKGGK-TTPFEDGSGRIOA 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 DKALGGTVTADPVSVSPGVJGNP-TDDEPVTKOLTTRNLGTGDVTLKLTSTATDFKGKAA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 THTFDUSGATEVTATLYMDYGEGSIDLYLYDPNGNEVDXSYTAXYGFENVGYXNPTAGTW 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 PAGEFILGATTVIVPA--- GGSASVDNTADFRLGGTVDGATSAYVVATGGGGTVRTAAAV 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 TVKVVSY------KINANYQVDVVSDGSLSQSGGNPNPNPNPNPNPTPTTDTOTF- 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 GREVESYDVIVRHIGRDGKPITZHLIDLIGYAGLASGRĞYG------APATDIATLR 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 KYGIRVINI,SLGSSQSSDGTDSLSQAVHN-AMDAGIVVCVAAGHSGPHTYTVGSPAAASK 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 VITVGAVDSKDNIASFSERGP-TADGRLKPEVVAPGVDIIAPRASGTSMOTPIND---YY 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 ALTVGÁVDDKÚKLÁDPSSTGPRLGUGAIKPDVTAPGVĎITAASABGNDIGOEVODCPAGY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   372 TKASGTSHATPHVSGVGALILQAHPSWTPDKVKTALIBTADIVAPKBIADIAYGAGRVNV 431
                                      Query Match 18.81, Score 647.5, DB 41. Length 570; DB 645. Length 570; DB 645. Length 570; Carell No. 26-38 177; Indels 85; Gaps Matches 179; Conservative 54; Mismatches 177; Indels 85; Gaps
                                                                                                                                                                                                                              140 TSVSQIGADTVWNSLGYDGSGV/VALVDTGIDANHPDLKGKYIGHYDAVNGRSTP--YDD 197
                                                                                                                                                                                                                                                                                                                                                                                                            198 QGHUTHVAGIVAGTGSVN-SQYLQVAPGAKLVQVKVLGADGSGSVSTIIAGVDWVVQNKD 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 VGHGTERVASTAAGTGAGSKGKÇKGKÇKOPPGAATLNGKVLDDSGPGDDSGTLAGKRAAAAO-- 116
                                                                                                                                                                                                                                                                                                           3 TSVGQIGAPKAN-SAGYDGKGVKIAVLDTGVDTSHPDLKGRVTA---SKNFTAAPGAGDK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICARY: Shih, Jason C.E.
APPLICARY: Lin. Xiang
APPLICARY: Lin. Xiang
APPLICARY: Miler. Eric S.COING BACILLUS LICHENITORNIS
ITILE OF INDEMITOR: PRO. KRATINOR
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COMPUTER: IBM PC COMPACIBLE
OPPRAFILES: TEM PC COMPACIBLE
SOPTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03,7250,028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSE: Kenneth D. Cibley
STREET: Post Office Drawer 34009
CTTY: Charlotte
STATE: NO. 5712147th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/03625774 Patent No. 5712147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          457 LPKGTYLVUSWIAKDFGT: 415
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URRENT APPLICATION DATA
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COMPUTER READABLE FORM:
NEDTUM TYPE: PLOPPY
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CORRESPONDENCE ADDRESS:
ADDRESSE: Kenneth D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
FILING DATE: 27-MAN
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US-08-685-774-2
15-03-000-016-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          563 KGTYLVDSWIAKDPOTLKGGIDWLVQPKLSVIKDF-TLTLDARTTKAADIIVPDPK---- 717
                                                                                                                                                                              374 ASGTSMATPHVSGVGALLLQAHPSWTPDKVKTALIETADIVAPKELADIAYGAGRVNVFK 433
                                                                                                                                                                                                                                        434 AIX----YDDYAKLFFTGSVADKGSATH 457
                                                                                                                                                                                                                                                                                                                                                                                                                                         495 ALQOTVIADPVSVSFCVQOMPHTDDEPVTKOLTYRNLGTQDVTLKLTSTATDPKGKAAPA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                458 TPDVSGAFFVTATLVNDTGSSDIDLYLYDPNONEVDYSYTATYGFEKVGYNPTAG7MTV 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 GFFILGATTVIVPA---GGSASVDWTADTRLGGTVDGAYSAYVVATGGGGTVRTAAAWOR 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S18 KVVSY-----KGAANYOVDVVSDGSLSQSGGGNPNPNPNPTPTTDTQTF--- 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  612 EVESYDVIVRHIGRDGKPTTEHLIDLIGVAGLGSGRÖYG------APATDIATLRLP 662
318 TVGAVDSKDRIASFSBRGP-TADGRIKPEVVAPGVDIIAPRASGTSMGTPIND---YYTK 375
                                                          COMPINE PROPAGE FORE:

COMPINE TEST DISKNETE. 35 Inch, 1.44 mb
COMPINE IBM COMPALABLE
OPERATING SYSTEM: MS-DOS
SOFTWARE NOTORMORE FORE 5.

CURRENT APPLICATION DATA.
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Patent No. 6143541
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TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEC ID NO: 7:
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LENGTH: 520 amino acids
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STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
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US-09-000-016-7
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Ower Watch
Best Local Smillerity 15,031 Score 560.5: DB 1. Length 379;
Matches 150; Conservative 0.93 Feed No. Zeo.32, Indexs 49; Gaps 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 AY------VEEDHVANALAQTVPYGIPLIKADKY-OAQGFKGANVKVAVLJTGIQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 ANHPDLKGKVIGHYDNVKGRSTPYDDQGHGTNVAGIVAGTGSVNSQYIGVAFGAKLVGVK. 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 VLGADGSGSVSTIIAGVDHYVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVHNAKDAGI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 VLNSSGSGSYSGIVSGIEMATIN----CHDVINNSLG---GAGGSTANKQAVDNA-RAGV 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 GYDIIAPRASGTSMOTPINDYYTKASGTSMATPHYSGYGALILQAHPSWTPDKYKTALIE 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 G------AGVESTYPINTYAT-LNOTSHVEDHVAGAAALLISKHPNLSASGVRNELSS 356.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIWA TYRE: Ploppy disk
COMPUTER: IBM PC COMPUTIBLE
OPERATING STSTEM: PC-DOS/MS-DOS
SOFTWARE: PREMETLE RELEASE #1.0, Version #1.25
CORRECT APPLICATION DATA:
                                       REDISFACTOR (NUMBER: 31,665
REPERSOC.FOCKER WINDER: 503,250
TELECOMMUNICATION INFORMATION:
TELETOM (19,9 02-2200
TELETOR (19,9 081-3175
TELETOR (19,9 081-3175
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                           NY POTNETICAL: NO
ORIGINAL SOURCE:
ORGANISH: BELLIUE licheniformis
STRAIN: PMD-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                410 TADIVAPKEIADIAYGAGRUNVYKA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 TATYLG --- SSFYYGKGLINVERA 377
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2-07-923-260A-4
: Sequence 4. Application US/07923260A
: Patent No. 5719021
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
                                                                                                                                                            LENGTH: 379 amino acids
TYPE: amino acid
                                                                                                                                                                                TYPE: TOPOLOGY: Linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                   REGISTRATION
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2IP: 19102
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MESSLY, 196-843-738, 1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 NQBVDTVIMEGSYGDRDRAVK - VLRLAGAQVKYSYKIIPAVAVKIKARDLLLIAGNIDT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 GYFGNTRVSGIKFIQEDY KVQVEGAT...SVSOIGADTVHNSLGYDGSGVVVAIVD7GIO 171
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APPLICATION NUMBER: 03/07/923,260A
FILING DATE: 31-JUL-1892
CLASSIFICATION: 435
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ANTI-SENSE: NO
ORIGINAL WOUNCE:
ORGANISM: Bacillus licheniformis
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INCOMMATION FOR SEQ ID NO. -1-
SEQUENCE CHARACTERISTICS
LENGTH: 300 manino actid
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LOCATION: 1.76
GTHER INFORMATION: A
US:07-923-260A-4
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HOLECULE TYPE:
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

DM procein - protein search, using sw model Run on:

October 31, 2002, 13:27:48; Search time 17 Seconds (Without alignments) 3724.875 Million cell updates/sec US-09-841-553-1 3437 1 WRRIGAVVLALVLVGLLAG7.......YAYSTYGWADYQLXAVVYYG 659 Perfect acore: Sequence:

283138 seqs, 96089334 residues Scoring table: BLOSUMS2 Gapop 10.0 , Gapext 0.5

283138 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 00 Maximum Match 1004 Lieting first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

plant plant Detabase :

Pred. No. is the number of easults predicted by chance to hive a significance control of the result below princed, and is derived by analysis of the cold score distribution.

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A/CCOSTRÉGRENCES: GB:299113, ÇW:ALA09126; NID:92634090; PIDN:CNB13610.1; PID:ell833 Séperimental Bource: Strain As C:Genetics: A)Stetus preliminary: nuclei. sold sequence not shown; translation not shown Avolecula type: DM Amesidues: Lidy cture.

C.Superfamily: subtiliain homelogy F:146-398/Domain: subtiliain hemology <SBT>

127 PIGEDYKVQVDDATSVSQICARRINSLGYDGSGYVVALVDTGIDANHPDLKGKVIGWYD 186 116 YLNREVRALLOFATEASH-ARIYVRAGOTLIGKGVTVAVVDTGI-YPHPDLEGRIIGGAD 173 Money March 19, 35°, Score 569-5; DB 2; Length 442; Marches 131; Conservative 21; Hanches 131; Conservative 21; Hanches 1699; 246 AGYDNYVO-NKDK--YGIRVINLSLGSS---OSSDGTDSLSQAVNNAMDAGIVVCVAAGN 299 234 EGVENCIQENEDRADEPIDITENES/GGGALREDHEGEBELVRAVERANSAGIVVCVAAGN 293 300 SGBNTYTVGSPAAASKVITVELSN-SN-----DNIASFSSRGPTADGRLKPEVVAPGUD 352 294 SGPDSQ71ASPGVSEKVITYGALDONNTASSDDTVASFSSRGPTVGKEKPDIIAPGVN 353 ò 음 5 8

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'73:995963; PIDN:RAAG6157.1: PID:9995964
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431 VYKA 434
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·Gaps Query Match 14.8h; Score 510; D8 1; Length 1433; Best Local Ballarity 26.4h; Pred. No. 50-70; Matches 210; Conservative 104; Mismatches 302; Indels 178;

8 RLISSVLSTVVISSLLFPGAAGASSKVISPSVKKELQSAESIONKISSSLKKS-PKKKEK 66 3 RLGAVVLALVLVGLL----AGTALANPVKPVVRN-----NAVOOKNYGLLTPGLFKKVOR 53 ô a

67 TTF-----LIKFKDLANPEKAAKAAVKKAKSKKLSAAKTEYOKRSAVVSSLKVTADESO 120 103 RDLLLI ------AGM1DTGY ------PGN 119 54 MMWNOEVDTVINFGSYGDRDRAVKVL-----RLHGAQVKYSYKIIPAVAVKIKA---- 102 q ò

121 ODVLKYLNTOKOKGNADOINSTYVVNGIAVHASKEVNEKVVOFPEVEKVLPNEKROLFKS 180 g

20 TRVSGIRFIGEDYKVQVDDATSVSQIGADIVWNSLGYDGSGVVVAIVDTGIDANNPDLKG 179 SSPFINKKAGKALKATDGVERNVDQIDAPKAW-ALGYDGTCVASIDTGVENNHPALKE 139 ò

180 KVIG------WYDAVNGRSTPYDDQCWCTHVAGIVAGTGSVNSQYIGVAPGA 225 a ò

240 KYRGYNPEHPNEPENENNHYDAVAGEASPYDDLAHGTHVTGTWYGSEPDGTNDIGVAPGA 299 226 KLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKYG-----IRVINLSLGSSQSSDCTDS 278 ò

300 KWIAVKAFSEDG-GTDADILENGENVLAPKDAEGNPHPENAPDVVNNSWG---GGSGLDE 355 279 LSGAVNNANDAG-IVVCVAAGNS-----GPNTYTVGSPAAASKVITVGAVDSNDNIASF 331 ò

356 WYRDWYNAWRAADIFPEFSAGNIDLFIPGGPG--SIAHPANYPESFATGATDINKKLAD? 413 332 SSRGPTADGRIKPEVVAPGVDIIAPRASGTSMGTPINDYYTKASGTSNATPHVSGVGAL: 353 a ò 8

392 LQAHPSWTPDKVKTALIETADIVAPKEIADI---AYGAGRVNVYKAIKYDDYAKLTPT3S 438 166 KOANASLSYDEMEDILTSTAEPLTDSTPDSPNNGYGHGLYNAFDAV-----SA 514 ò

572 KLDGGEWTEITAKRISGDHLKGTYQAEIPDIKGTKLSYKWMIHDFGGHYVSSDYYDV7VK 63, 449 VAD-KGSATHIFDVSG-----ATFVTALLYWDIGSSDIDLYLYDPHGNEVDYSYTARY 53C 515 VIDGLGKAEGQVSVEGDDQEPPVYQHEKVTEAYEGGSLPLTLTAED---KVSVTSVKLSY 571 501 GPEKVGYYNPTA-----GTWTVKVSYKGAANYQVDVVSD--GSLSQSGGNPNPN 549 g g ò ò

PSITAGYKODFETAPGGHVASGTNHHMEKGVPSTGPNTAASGEKVYGTNLTGNYA---- 686 599 NDLDLYLYDP-----NGNLVDRSTSSNS-----YEHVEYANPAPGTWTFL-VYAYSTY: 645 587 NSANNNLVMPPIKAPDSGSLPLQFKSWHNLEDDFDYGYVFVLPEGEKNWBQAGVYNGKTS 746 550 PNPNPTPTTDTGT----FTGSVNDY-HDTSDTFTMNVHSG----ATKITGDLTFDTSY 598 632 à ò

646 GWADYOLKAVYYYG 659 SWIDEEIDLSAYKG 750 747 ò

RESULT 15

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A: Accession: A41448 A: Molecule type: DNA

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Accessing 1581 and 6000044; NID-0215538; PIDN: MANDIAG. 1; PID:951245 Accessing research of DODOS44; NID-0215538; PIDN: MANDIAG. 1; PID:9512425 Accessing 1582 and 15

Noblocule Upper protein A. Molecule M. Molecule A. Molecule A/Title: Isolation, characterization and structure of subtiliain from a thermostable A/Reference number: \$88012, WiD:96069945 AAcession: 680812

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A Service codes (FG)

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Gaps Indels 49; Query Match
14.5% Score 309.5; DB 1; Length 381;
Best Local Similarity 37.3%; Predd No. 156-20;
373; Conservative, 54; Mismatches 124; Indels 49,

13

78 VLRLMGAQVKYSYKI1PAVA: KIKARDLLLIAGMIDTGYPGNTRVSGIKPIQEDYKVQVD 137 58 VISENGGKVOKOPKYVNAALA/LDEKAVKEL-----KKDPSVAYVEEDH-IAHE 105 138 DATSV----SQIGADTVANSLCYDGSGVYVAIVDTGIDANHPDLKGKVIGHYDAVNGRST 193 â à

222 SN----NADVINASLG---GPSGSTALKTVVDKAVSGIVVAAAAGNEGSSGSSGVGYP 274 153 PYODGSSHCTHVAGTIAALHT SIGVLGVSPSASLYAVKVLDSTGSGGYSWIINGIEWAI 221 253 GNKDKYGIRVINLSLGSSQPSUGTDSLSQAVNNAMDAGIVVCVAAGNSGP--NTYTVGSP 310 용 ò 윱

371 YTKASGTSMATPHVSGVGFLILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVN 430 311 AAASKVITVGAVDSNDNIAWFSSRGPTADGREKPEVVAPGVDIIAPRASGTSMGTPIHDY 370 275 AKYPSTIAVGAVNSSNORASFSSAGSELD-----VNAPGVSIQSFLPGGT----- 319 YGAYNGTSKATPHIVAGAAALILSKHPTWTNAQVRDRLESTATYLG----NSFYYGKGLIH 375 Ξ 330 8 à à 용

VYKA 434 VOAA 379 376

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OM protein - protein search, using sw model Run on:

October 31, 2002, 13:25:28 : Smarch time 10 Seconds (Without alignments) 2351.618 Million cell updx:385/8ec US-09-841-553-1 Perfect score:

1 HERLGAVVLALVLVGLLAGT......TAYSTYGWADYQLEAVVYYG 639.

Sequence:

105224 seqs, 38719550 residues Gapop 10.0 , Gapoxt 0.5 **BLOSUM62** Scoring table: Searched:

rotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

screet, No. is the number of results predicted by chance to have a server of seaser than or equal to the sorse of the result being printed, and is derived by analysis of the cotal score distribution.

SUMMARIES

	Description			P00782 bacillus am				1	004100 0001100	CHETTOR		Parson rectalus on	CE SUITIONS ACCUTA			P07518 bautilus on		Directions.	P04072 Post Creation		Par.			PSESOS PATOLOGICA		bact.l.		thermus s	becilins	achtana.		Daniel Line				P25036 saccharonyc	PS8371 magnaporthe	P54423 bactility 811	
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Laberg from Bacillus licheniformis. Tr. Nucleic Acids Res. 13:8913-8926(1985).

SEQUENCE OF 166-199.

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A-RAY CRESTALLOGRAPHY (2.4 ANGSTROMS) OF VARIANT WITH SELENCOFS-125 STORE (2.4 M. 2.4 M. 1.6 M. 2.4 X-BN CRYSTALLOCANNEY (1: ANGSTRONS) OF 106-379.

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SCOLL V. S. Eger B.T. F. The Market St. Co. Martichanak V., Jones J.B., Blochemistry 32:6157-61c+:1593).

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63; Gaps 14; and a Length 382; Indels Score 533.5; DB 1; Pred. No. 3.1e-23; 52; Mismatches 113; 38.5% Sest Local Similarity 38.5 Matches 143; Conservative Similarity Duery Match

101 DEVAHAYAQSVPYGVSQIKAPAL-HSQCTTGSNVKVAVIDSGIDSSHPDL--KVAGGASM-157-78 VLRLMGAQVXXSTKIIPAV-----AVXIKARDLLLJAGMIDTGYFGNTRVSGIKFIGE 130 VNGRSTPY - DDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLYGVKYLGADGSGSVSTIIA 246 158 VPSETNPEQDNNSHCTHVAGTVAALNN-SIGVLGVAPSASLXAVKVLGADGSGQYSWIIN 216 .69 305 YIVGSPAAASKVIIVGAVDSNDNIASFSSRGPIADGRLAPEVYAPGVDIIAPRASGISNG 35A 131 DYKVQVDDAT---SVSOIGADTVWNSLGYDGSGVVVAIVDTGIDANIIPDLKGKVIGHYDA 187 247 GYDWYYGHKDKYGIRYINLSLGSSOSSDGTDSLSQAVNNAWDAGIYYCYAAGNSGP--NT 104 887 용 ò a g à g ò

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370 YGKGLINYONA 380 \$24 YGAGRVNVYKA 434

15.007-2001 (Rel. 40. Created) 116.007-2001 (Rel. 40. Lags Sequence update) 01.40R-2002 (Rel. 41. Lagt Sequence update) PLS OR PFOJST, PROJECT (EC 3.4.21.-). PRT; 1398 AA. PLS_PYRFU

Archee; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus., NCBL_TaxID-2261; Pyrococcus furlosus.

SEQUENCE FROM N.A., SEQUENCE OF 150-184, AND CHARACTERIZATION. STRAIN-YOL / DMS 350-707 FUNNED-8702780;

Woodword W Gill, Breen R. C. L., Gebring A. C. M., Platteeuw C., Staten R. J., do Word K. L., Gebring C. W. C. M. S. Staten R. J., do Word K. L. Staten R. J. Gold Wood R. M. S. C. W. C. M. S. Staten R. S. Gold R. G. W. C. M. S. Staten R. G. M. S. Staten R. S. Staten R. S. Staten R. Sta

SUBTILASE PAMILY.

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InterPort 188000209; Peptidase_88.
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Glycoprotein; Zymogen; Signal POTENTIAL. 222 222 223 223 223 223 223 223 CARDOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD

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Cargett structure of citizities or a rendom mutent of subtilisin
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Bur. J. Stochen. 237:109-118(104).
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Best Local Similarity 42.7%; Score 524.5; DB 1; Length 274;
Best Local Similarity 42.7%; Profit No. 6.56-273
Marches 132; Conservative 38; Mismarches 94; Indels 49;
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ACLSITE 3 CHARGE RELAY SYSTEM.
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ACLSITE 220 CHARGE RELAY SYSTEM.
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Becirlus, Firmicutes: Bacillus/Closiridium group:
Bacillus/Staphylococcus group: Bacillus.
KGBI_TAXED-103;
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                                                                                                                                                        606 YDPNGNLVDRSTSSNSYEHVETANPAPGTWTFLVYAYS 643
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Subtilisin DY (EC 3.4, 21.62).
                                                                                                                                                                                                                                                                                                                                                                   274
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                                                                                                                                                                                                     Best Local Similarity 22.64; Pred. No. 1.6e-22;
Matches 239; Conservative 104; Mismatches 248; Indels 467; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 GAOIMAIRVLRSDGRGSMWDIIEGWTYAA----THGADVISHSLGGNAPYLDGTDPESVA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 VNNANDA-GIVVCVAAGNSGPNTYTVGSPAAASKVITVGAVD------323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 FGWDGRGHGTHVAGTVAGYDSNNDAMCMLSMYSGEWEVFSRLYGWDYTNVTTDTVOGVAP 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 -PYDDOGHGTHVAGIVAGIGSVN-----SOYI------GVAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKDKYGLRVINLSL-GSSQSSDGTDSLSQA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 VDELTEKYGVYFVIAAGNEGPGINIVGSPGVATKAITVGAAAVPINVGVYVSQALGYPGY 533
                                                                                                                                                                                                                                                                                                                                                                                                                58 ---QEVOTVIMFGSYGDRDRAVKVLRLMGAQVKYSYKIIPAVAVKI---KARDLLLIAGM 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 MKGOPNAVLIIKTKEGKLEEAKTELEKLGABILDENRYLNMLLVKIKPEKVKELNYISSL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 IDTGYFGNTRVSGIKFIQEDYKVQVDDATSVSQIGADTVHNSL-----GYDGSGVVVAI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 VDTGIDANH-----PDLKGKVIGWYD-------AVNG------190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 LDTGVDPHHPPLSITPDGRRKIIEWKOPTDBGPVDTSPSFSKVVNGFLIINTFGVASGL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 NSTCNGYDIAYVDTDLDYDFTDBVPLGOYNVTYDVAVPSYYYGPLNYVLABIDPNGEYAV 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 -----SNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDYYTHA 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 EKAWLNREVKLSP-PIVEXDVXTK-EPSLEPKMYNSTWYINALOPIOEPGYDGSGVVVAV 177
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                                                                                                                                                                                                                                                                                       2 KRLGAVVLALVLUVGLLAGTALAAPVKPVVRNAVQQ--KNYGLLTFGLFKKVORMWN 7: 57
                                                                                                                                                                                                                                                                                                                             4 KGLTVLPIAIMLLSVVPVHPVSAGTPPVSSBNSTTSILPNOQVYT----KEVSQAALMAI 59
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                                                                                                                                                                           DB 1; Length 1398;
1208 1208 N-LINKED (POTENTAL).
1237 1237 N-LINKED (POTENTAL).
1328 1337 N-LINKED (POTENTAL).
1338 A. 134499 N-LINKED (POTENTAL).
1398 A. 134499 N-LINKED (POTENTAL).
                                                                                                                                                                     15.5%; Score 533.5; DB 1; 22.6%; Pred, No. 1.6e-22;
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148 KDVŢISEDANSPONDS --SAPVIGANDAND-LGYTGKGIKVAIDDIGVEYNHPDIKKNFG 204
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                                                                                                     191 IVVCVAAGNSGPNIYTVGS-1,AASKVITVGA-
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
F98453BF00B653DD CRG64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.7; SCORE 522.5; DB 1; Length 806; Mast Local Similarity 24.17; Pred. No. 3.3e-22; Mass Local Similarity 24.17; Pred. No. 3.3e-22; Mass Local Similarity 24.17; Mismatches 208; Indels 269; Matches 208; Lindels 269;
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Subtilist, BG10591, vpr. ...
InterPro, IPR003137, PA.
InterPro, IPR000209; Peptirase_S8
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                                                                                                                                           47 GASTVSGESYNTDGNGHGTHVAGTVAALDNTTG-VLGVAPRVSLYAIKVLNSSGSGTVSA 105-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 -NTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPFADGRLKPEVVAPGVDIIAPRASS: 3617
                                                                                                                                                                                                                                                                                                                                                                   184 WYDAVNGRSTPYDDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADGSGSVST. 243
                                                                                                                                                                                                                                                                                       244 IIAGVDWVVONKDKYGIRVINLSLGSSQSSEGTOSLSQAVNNAHDAGIVVCVAAGNSGP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S GSQNTIGYPAKYDSVIANGAVDSNKNRASFSSNG-----ABLEVNAPGVSVYSTYPSNT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 SMGTPINDYYTKASGTSKATPHYSGYGALILQAHPSWTPDKVKTALIETADIYAPKELAD (21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 -----YTSCHQTSHASPHVAGAAALILSKYPTLSASOVRNRLSSTATNLGD----S
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WEDLINE-9264374; PURCH-1938992.
SLORE A., RUCO G.A. JF., Theriault K.A., Dwyer M., Wilson S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *Cloning and characterization of the gene for an additional attracellular series protease of Bacillus subtilis.";

*Recental 173:6895-6895(1991)
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Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID-1423;
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194 PYDD-GGHGTHVAGIVAGTGS7HSQYLGVAFGAKLVGVKYLGADGSGSVSTIIAGVDAVV 252
                                                                                                                                                                                                    163 PYODGSSHOTHWADTIALNESS COULON PSASLYNKYLDSTOSGOYSMILHOIDMAI 221
                                                                                                                                                                                                                                                                                                                                                          253 ONKDKYGIRVINLSLG-5GQSSNGTDSLSDAVNNANDAGIVVCVAAGNSCP--NTYTVGSP 310
                                                                                                                                                                                                                                                                                                                                                                                                                               222 SH-----NBVINNSLG----GPT-38TACKTVVDKAVSGGTVVAAAGNBGSGGSTSTVGPP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 AAASKVITVGAVDSHDWLASFSSRCPTADGRLKPEVVAPGVDIIAPRASGTSHGTPINDY 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 YTKASGTSHATPHYSGVGKLILQAHPSHYPDKVKTALIETADIVAPKELADIAYGAGRVN 430
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376 VQAA 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 VLRLMGAQVKYSYKIIPAVAVKIKARDILLIAGHIDTGYFGNTRVSGIKF1QEDYKVQVD I37
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Live 52; Mismatches 124; Indels 49; Japs
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Pun Protosis - perlama-18-
Pun Proto
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Bacillus/Staphylococcus group: Bacillus.
NEBI_TEXID-86019;
                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Leat Begunce update)
15-DEC-1998 (Rel. 37, Last Benckatlon update)
Subtiliain NAT precureor (BC 3.4.21.62).
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38-2%; Pred, No. 4.2e-22;
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107 381 SUB
138 138 CNA
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381 AA; 39507 MH; C
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EMBL, S51909; AAC60424.1;
PIR; JH0778, JH0778,
HSSP; P07518; JHSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis var. natto.
                                                                                                                                                                 STANDARD;
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Watches 139; Conservative
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                                                                                                                                          SUBN_BACHA
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                                  RESULT 6
SUBN_BACNA
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-- SIMILMATTY: BELOANS TO PEPTIDASE PAMILY 58; ALSO KNOWN AS THE
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15-CATON (Rel. 10, Last Sequence update)
15-CA
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Jr., Rudolph C.P., Sullivan B.J., Theriault K.A.,
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SF73ABC68D586831 CRC64:
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Bacillus/Staphylococcus group; Bacillus.
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   SEQUENCE FROM N.A., AND SECUENCE OF 195-222
MEDLINE-90170864; PubMei-1105512;
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                                                                                                                                                                                                                                                                                                                                                     97 ------PAISYIREDAEVITMAOSVPHGISRVQAPAAHNR-GLIGSGVKVAVLDIGI-S 147
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                                                                                                                                                                                                                                   116 YFGNTRVSGIKFIQEDYKVQVDDAT---SVSQIGADTVWNSLGYDGSGVVVAIVDTGIDA_17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 NHPDLKGKVIGHYDAVNGRSTPYDDQGHGTHVAGIVAGTGSVNSOYIGVAPGAKLVGVKV:232
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Microcogonisms in albaling evicomenta, pp.187-184, VCH,
Moinbell (1991).
- SUDCELUJAK LOCOTION: Secreted.
- SUDCELUJAK PRILOKNS TO PEPTIDASE PANILY 88; ALSO KNOWE AS TWE
SUPTILASE PANILY.
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PRALIMENDOLS) / APRC 2155/2 / 2004 9139 / DSM 5312;

PRALIMENDOLS) PROMOGRAPH M., NORMARIA S.,

TABREL M., NORMARIA PROGRAMS REALINGS AND SERVICES AN
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01.40V.1555 (eb. 13. Latt squaree update)
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STRAIN-221 / ATCC 21522 / JCM 9139 / DSM 2512;
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S48754; AAC60420.1; -. EMBL; D1357; BAA02442.1; -. EMBL; A26817; CAA01836.1; -. EMBL; A22569; CAA01611.1; -- HSSP; P29600; 1GC1.
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XIONEN > N (IN REF 3).
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ADWAYNON > PERSRICS (IN REF 3).
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Conservative 104; Mismatches 302; Indels 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 YAQSYDSGISQIKAPAL-HSGGYTGSNVKVAVIDSGIDSSHPDL--NVRGGASFVPSETN 162
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Bacillus Pirmicutes: Bacillus/Clostridium group;
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which are 7.5, Worlham w., Settle E.L.;
Subcillish Maylosocheriticus I.I. Solation and sequence of the rippic and opnosen bronde peptides. T. 1. Solation and sequence of the rippic and opnosen bronde peptides. T. 3. Solation. 247, 5602-5618 (373).
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CHARGE RELAY SYSTEM (BY SIMILARTY).
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POTENTIAL.
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15-DEC-1998 (Rel. 37, Last annotation update)
Sub-Lilistn emylosacchariticus precursor (BC 3.4.12.62).
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Bacillus/Clostridum group;
Bacillus/Staphylococcus group; Bacillus.
WCB_TAXID-183;
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Tem PP000215; Peptidase_88: 1.
RRINTS; PR00721; SUBTILISIN
RESITE; PS00116; SUBTILARE_ASP_1.
RROSITE; PS00117; SUBTILARE_ASP_1.
RROSITE; PS001180; SUBTILARE_ASP_1.
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PIR: A41448; A41448.
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P00783;
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T. C. Complete Months and Service Medical Amorphise Service Inc. Complete Months and Service Medical Amorphise Serv
**Complete amino acid seguence of alkaline mesentericopeptidase: 
***Sebtlisti isolated from interain of Bacillus mesentericus.*; 
FBBS Lett. 196:218-234(1883);
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BY SINILARITY.
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Rem. PR00023; SQUFILIS;R
PRNTS; PR00723; SQUFILIS;R
PROSTE; PS00136; SUBTILIS;R
PROSTE; PS00131; SUBTILIS;R
PROSTE; PS00131; SUBTILIS;R
PROSTE; PS00131; SUBTILIS;R
PROSTE; PS00138; SUBTILIS;PS00138; SUBTILIS;PS001
                                                                                                           X-RAY CRYSTALLOGRAPHY (2.5)
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MEROPS; S08.002; -.
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      use by non-profit institutions as long as its octent is 1% ino vay modified and this statement is not removed. Usage by and for conservable estitics required a license agreement (See http://www.isb-sib.ch/ensounce/or send an easil to licensetiab'sb.ch/ensounce/
for commercial
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SUBTILIZEN J.
CHARGE RELAY SYSTEM (BY STHILARITY).
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54; Mismatches 124; Indels 49;
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01-APR-1988 (Rel. 07, Last sequence update)
16-CC*-2001 (Rel. 40, Last sequence update)
Subtilisio (RC 3.4.21.62) (Alkaline mesentericopaptidase).
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PRINES, PROMODE, Pettidane, St.
PRINES, PROVINS, STRILLESH.
PROSTER, PROVINS, STRILLES, ESPA, DEPRENTAL,
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PROSPERTAL.
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Bacteria: Rimicutes; Bacilius/Cistridium group;
Bacilius/Stabhylococcus group; Bacilius.
WCBL.TaxID-1408;
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37.5%; Pred. No. 7e-
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AC P07518;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 USQIGADTVMHSLGYDGSGVVVAIVDTGIDANHPDLKGKVIGHYDAVHGRSTPYDD-OGH 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 RYTHISLGSSOSSOCTOSLSGAVNRAMDACLYVCVAAGNSOP--NTYTVGSPAAASKVIT, 518
120 DYIHNSLG---GPTGSTALKTVORGAVSGITVAAAGNSSSSGSSVOCTPAKTPSTIA, 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 YGAVDSHDMIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSMGTPINDYYTKASGTS 378
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                                                                                                                                                                                                                                                                                                                                                                                                                              99; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 ISOIKAPAL-MSOGYTGSMVKVAVIDSGIDSSHPDL--NVRGGASFVPSETNPYGDGSSM 64
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Characterization of an alkaline elastase from alkalophilic Becillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 MATPHUAGAALILSKHPTHTHAQVRDRLESTATYLG----SSFYGKGLINVQAA 2733
                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 275;
                                                                                                                                                                                                                                                                                                                     27655 MM; 338DA897DBA4170A CRC64;
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Bacienis/Firmicutes: Bacillus/Clostridium group:
Bacillus/Staphylococcus group: Bacillus.
HGBL-Taxib-1409;
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VEPEB-1951 (Rel. 17, Leat sequence update)
16-CT-2001 (Rel. 40, Leat sequence update)
Alkeiing elestese Yes precursor (EC 3.4.21..)
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274
275 M.:
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CHARGE RELAT SYSTEM (BY SIMILARITY).
SABFDSCCOCG2687D CRC64; ALKALINE BLASTASE YAB Principton Impulsons and American Services and American Propertions and American Services and American Service 141 141 CHA 171 171 CHA 324 324 CHA 378 AA, 38793 HR, EMBL: M28537; AAA87324 3: -. HSSP, 099405; 1MPT.

49 VDOI-----DGDEYSISSARDVELDHEPDFIPVLSVELDPEDVDALE--LD----- 95

120 TRVSGIKFIQEDYXVQVDDAT··SVSQIGADTVWNSLGYDGSGVVVAIVDTGIDANHPDL 177 96 ---PAIAYIEEDAEVITMOTVPWGINRVQA-PIAOSRGFIGTGVRVAVLDIGI-SNHADL 1S0

298 GNSCPNTYTVGSPAAASKVTTVGAVDSNDNIASFSSRCPIADGRLKPEVVAPGVDIIAPR 3S7 261 GNSGAG--NVGPPARYANAMAGSTDONNNRATFSQYGAGLD-----IVAPGV----

358 ASGISMCTPINDYYTKASGISMATPNVSGVGALILQAHPSWTPDKVKTALLETADIVAPK 417 307 --GVGSTVPGNG-YASPNGTSHATPHVAGVAALVKOKNPSWSNVQIRNHLKNTATNLG--

362 -- NTTOPGSGLVNAEAATR 778

01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
M-procease (EC 3.4.21.) 269 AA PRI, STANDARD:

Bocillus sp. (strain KSH-416). Becteria: Firmicutes: Bacallus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.



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SIMILARIT: BECONS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SUBTILASE FAMILY.
                                                                                                                                                                                                                     Y., Adachi S., Hitomi J., Yoshimatsu T.,
                           "ANY CRESTALLOGRAPHY (2.4 ANGSTROMS).
Yeaner T. KRAT F. We Bennad T. Sprakit A., Ashida T.,
Choopeahi T. Ito S. Temshira O.:
Serrotter of a new sellaline merime protease (W-protease) from
Serrotter of a new sellaline merime
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7A03C66D534A1D07 CRC64;
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                                                                                                                                                                            SEQUENCE OF 1-23, AND CHARACTERIZATION. REDLINE-95356832; Pubmed-7532397;
                                                                                                                                   cta Crystallogr. D 51:199-206(1995).
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Best Local Similarity
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PROSITE: PS00137;
PROSITE: PS00136;
WCBL_TaxID-1409;
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Duery Watch
14.21; Score 488.5; nb 1; Length 269;
18sst Lober Similarity 41.44; Pred, No. 66-21;
18sst Conservative 43; Mismatches 97; Indels 33; CapeMatches 122; Conservative 43; Mismatches 97; Indels 33; Cape142 VSQIGADTWANSLATICSGVYVAIVDTGIDANHEDLAKKVIGHTDAYNGRSTPEDOQUE; 20).

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10 sp.phant:
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14 sp.unclassified:
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	Murphy L., Harris D.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases [12]	- 1,77	Thomson N.R., Parkhill J., Barrell B.G., Rajandroom M.A.:	> the EMBL/GenBank/DDBJ datobe	171		ed-3463436;	Redenbach M., Kleser F.M., Denspalte D., Elchner A., Cullum J.,		A set of ordered cosmids and a detailed genetic and physical map for	non-looka Alina absorbed
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Babutted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 1911; CASI3510,17 - .
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Matches 151, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                72 RDRAVKVLRLMGAQV------KYSYKIIPAVAVKIKARDLLLIAGMIDIGYFGNWWW 122
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                                                                                                                                                                                                                                                                                                                                                  67; Mismatches 134; indels 50;
                                                                                                                                                                                                                       Juery Match 20.34; Score 699; DB 2; Length 1245; Sest Local Similarity 41.14; Pred. No. 66-28; Matches 175; Conservative 67; Mismatches 134; Indels SO
          PRINTS: PRO0723; SUBTILISIN.
PROSTIE: PSO0137; SUBTILASE.HIS; UNKNOWN_1.
PROSTIE: PSO0138; SUBTILASE.ESR; 1.
SEQUENCE 1245 AA; 130895 WM: 74EE92DB9CAlde6 CRC64;
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001788 (TEDSLEE) 05, Greated)
01-VAN-1998 (TEDSLEE) 05, Last Sequence update)
10-VAN-1998 (TEDSLEE) 105, Last Sequence update)
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Bacilius, Plimicutes; Bacilius/Clostridium group;
Bacilius/Staphylococcus group; Bacilius.
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SEQUENCE FROM N.A.
STRAIN-168;
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176 DLKGKVIGWYDAVHGRS?PP -- DDQCHGTHVAGIVAGTGSVN-SQYIGVAPGAKLVGVKV 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 F----TGSVADKGSATHT------FDVSGATFVTATLYWOTGSSDIDLYLYDPNGN 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1102 AA: 114,128 MW; F9E4AD2590FE559E CRC64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 SQIGADTVWNSLGYDGSGVVVAIVDIGIDANHPDLKGKVIGWYDAVNGRSTPYDDGSHGF 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         316 VITVGAVD-----SNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGT----SN 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 GIRVINLSLGSS----OSSDGTDSLSGAVNNAMDAGIVVCVAAGNSGPNTYTVGSPAAASK 315
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SHELF, PRODISTJ, RANGSE(9.1).

SHESPS, 0984651 IMP.
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NEDLING-00125 / DUNG-1108812;
NETH WARGOOR TO TAKANI Y. MAGNO G., Sasaki R., Magui N
FUJI F., Hirama C., Nakamara Y., Dagaswara N., Kuhara S.,
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TREETO, TROOLIGA (C.P.48)
TREETO, TROOLIGA (C.P.48)
TREETO, TROOLIGA (C.P.48)
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01-WAY-1997 (TEBMBLEB. 03, Last sequence update)
01-DEC-2001 (TEBMBLEB. 15, Last annotation update)
SUBTILISIN-LIKE PROFENCE.
Bacteria: Firmicutes: Bacillus/Clostridium group:
Bacillus/Staphylodoccus group: Bacillus.
BacillustiD-86665;
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                                                  133 KAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLYKDTGSSDIDLYL 484
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BEST LOCAL SIMILATITY 16.4%; Pred. NO.4.86.78; Indels
BEST CONSERVATIVE, (,8); Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cerdeno A.M., Parkhill J., Rarrell D.G., Rajandream N.A.
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                               UTATIVE SECRETED PEPTIDASK.
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41.5%; Pred. RO. 3.5e-25; Indels 35; Geps 11;
Live 52; Wissmatches 129; Indels 35; Geps 11;
ACC. 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 GAQVRYSYKIIPAVAVKIKARDELLIAGMIDTGYFGNTHVSGIKFIGED--YKVQVEDAT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 GGSIMPEIPLIKGWSVNLPCDKLKHPAS-----INGIHPLAEDSLVKLQLHIAT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 SVSOIGADTVWNSLQYDGSGVVVAIVDTGIDANHPDL---KGKVIGWYDAVNGRSTPYND 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 GGHGTHVAGIVAGTG-SVNSQYIGVAPGAKLVGVKVLGADGSGSVSTIIAGVDWVVQNKD 256
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A novel subcliberilies estim protease from Thermouneschacter
yonselessis (8-1: Cloning, expression and bicohemica, properties:
spinited (MMR-2001) to the EMBL/GenBank/DOBJ databases.
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"A set of ordered commiss and a distilled genetic and physical map for
the 8 No Streptonyeas occilcolor Al(2) chromosome."; J.T.77-96(12)
R.M. Ercobolo. J. 177-796(12)
R.M. Ercobolo. J. 177-796(12)
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R.M. Ercobolo. J. R.M. E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 IDANHPOLKGKVIGHYDAVNIHKSTPYDDQGHGTHVAGIVAGTGSVNS-QYIGVAPQAKLV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 GVKVLGADGSGSVSTIIAG@UbFNQNKDKYGIRVINLSLGSSQSSDGTDSLSGAVNN-AW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 DAGIYYCYAAGNSCPNTYT: $20PAAASKVITYGAYDSNDNIASPSSRGPTADGRLKPEVV 347
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Actionopostals firmicures, Actionobacteria, Actionobacteridae
Actionopostalas Streptonycinase: Streptonycasaceso; Streptonycas.
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REDLING-9700031; Pubmed-8843436;
Redenbach M., Kleser H.M., Denspeite D., Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sourcy March
Bone Cocal Similarity 22.16* Pred No. 2.46*22. Access Watches 172; Conservative 74; Misaacchea 182; Indeas 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-A3(2):
Cerdeno A.M., Parkhill J., Berrell B.G., Rajandream N.A.;
Submitted (AUG-2000) to the EMBL/GenBank/Dobi databases.
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Squiders D.C., Marris D.
Submitted (AUG-2000) to the DMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001 (PrBHBLEAL 16, Created)
01-WAR-2001 (PrBHBLEAL 15, Last asquence update)
01-DEC-2001 (PrBHBLEAL 19, Last annotation update)
PUNITYE SECRETED PERFISSES.
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539 DVTYTNSGPAPVALDLAIGPASLPEG---
                                                                                                                                                       524 GAAN----YQVDVVSDGS 537
                                                                                                                                                                                                                         590 DAAEDNGAYATRLVASGA 6.07
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Limin II, the Description of the Control of th
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Best Local Statistity 37-44 Feed No. 73-5-34;
Matches 164; Conservative 777 Hismatches 160; Indals 47: deps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 GGRLAGGLAKWALDGKVRATLSDTTAQIGAPDWHSG-GNTGEGVGVAVLDTGVDKREPE_557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 GSGQDSHYLAGHENAVBQR---AKIVSHSLGDS-PTDCTDPLSEAVN--NLSAETGALE 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294 CVAAGUSGPHTYTVGSPAAASKVITVGAVDSN----DNIASFSSRGP-TADGRLKPEVVA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 VVANGUSGPEATTVGTPAAADAALTVGAVNGPGKGVDOLADPSSRGPRVGDNAVRPDILLR. 430
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Actinopacterias; Streptomycinose; Streptomycetaceae: Streptomyces;
NCBI_Taxib-195;
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Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                         01-MA-2001 (Tribulatel. 16, Created)
01-MA-2001 (Tribulatela. 16, Last sequence update)
01-MC-2001 (Tribulatel. 19, Last annotation update)
PUTATUS SCRETED PEPTIONSE.
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                       PRELININARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor
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125 IKPIQEDIKVQVDDAT---- SVSJIGADTVKNSLGYDGSGVVVAIVDIGIDANHPDLKGKV 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 VGGASFVAGGARYTDGWCHGTN/AGTVAALDNTTG-VLGVAPSVSLXAVKVLHSSGSGSY 208
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          360 GISMCTPINDYYTKASGISMAT?HVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEI 419
                                                                           316 ST-----YATLNOTSP/30-AVADAAALILSKEPNLSASOVRNRLSSTATVLG---- 362
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374 374 374 Mr. B61432A1B42C526E CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Lest sequence update)
01-MR-2001 (TrEMBLrel. 18) Last sencetation update)
SUBTILISIN PRECURSOR (EC 3.4.21.62) (FRAGHENT)
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Bacillus/Stabhylococcus qcohp; Bacillus.
NCBI_TaxiD=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 AA
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                                                                                                                                                                                                                                 420 ADIAYGAGRUNYYKA 434
                                                                                                                                                                                                                                                                                                                      363 SSFYYGKGLINVEAN 377
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STAINGOOD LITTOR E.K. Lies T.E. Master E.S. On J.;
STAINGOOD LITTOR E.K. Lies T.E. Master E.S. On J.;
Machine I.G. Good of Mark game encoding a strationytic processe of
machine Interaction of V.IAT. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 IGHYDAVNORSTPYDDQGHGTHVAGIVAGTGSVNSQYIGVAPGAKLVGVKVLGADK-138V 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 VGGASPVAGEAY WIDGNCHGTHVAGTVAALDWITG-VLGVAPHVSLYAVKVLNSS: 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 STILAGUDWYVQHKDKYGIRVINISLOSSQSSDGTDSLSQAVHNAWDAGIVVCVAZINSG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 SQIVSGIERATIN---GRDVINMSLG---GPSGSTANKGAYDNAYARGVVVAAAG-660 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 SSGNTNIGIPAKYDSVIAVGAVDSNSNRASFSSVG-----AELEVAAPGAGVST.F--315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 GSYGDRDRAVK--VLRLMGAQVKYSYKIIPAVAVKIKARDELLIAGMIDTGYFGNTFVSG 12A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.4%; Score 564.5; DB 2; Length 379;
35.6%; Pred. No. 1.18-21;
i.ve 61; Mismatches 144; Indels 75; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 KS-GVKTASVKKDIIKESGGKVDKOPRIINAAKAKLDXBALEEVKNDPDVAK------95
429 APCVGILAANSSFAAGG---NGAYQSLSGTSMATPHVAGAAALLAAARPDLSGSALK--- 482
                                                                                                408 IETADIVAPKEIADIAY-----GAGRVNVYKAIKYDDYAKLTFTGSVADKGSATHTFDVS 462
                                                                                                                                                                                      483 ----DVLASSSHRTPRYDAFQAGSGRYDVDAAVRAGVYASATAYAPGSSPGPVRRLVTY 538
                                                                                                                                                                                                                                                                                      463 GATPVTATLYWDIGSSDIDLYLYDPNGNBVDYSTTAYYGFEKVGYYNPTAGTWTVKVYLY 522
                                                                                                                                                                                                                                                                                                                                                                                       539 NITGMAVIL.....BLSVAATBAPE.-GVFRLSASRVIVPA--- 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 KGAANYQVDVVSDGSLSQSGGNPNPNPNPNPTPTTDTGTFTGSVNDYHDTSDTFTHNVN 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        573 HGTAD -- VILTIDGSGSAGG-----RAYSCOIL----ATDADARS'A 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VYLALVLYGLLAGTALAAPVKPVVRNNAVQQKNYGLLTPGLFKKVQRMNNQEVDTVINF 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 MITALMINPTHAFEDSASAAQPAK-----NVEKDYIVOF 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 HTAVS-AGPVR-----HKLTVHFKDADG-------NPVPGVFDLL $40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        583 SGATKITGDLIFDTSYNDLDLYLYDPNGNLYDRSISSNSYEHVEYANPAPGTWIFL 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2001 (TIEMBLIEL 16, Created)
01-WAR-2001 (TIEMBLIEL 16, Last sequence update)
01-08C-2001 (TIEMBLIEL 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus licheniformis.
Bacillus/Clostridium group:
Bacillus/Csaph/lococcus group: Bacillus.
Ksa.Tax.D=1402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 379 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 35.6%
Matches 155, Conservative
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Bacilius licheniformis.

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Query Match 16.3% Score 559.5; DB 2; Length 379; DB 2sc Local Statistity 31,74, Pred( No. 1.99-7); Indela 49; Caps Matches 133; Indela 49; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 NQEVDTVINFGSYGDRDRANK - - VLRLAGAQVKYSYKIIPAVAVKIKARDLLLIAGNIDT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 GYPGHTRVSGIKFIOEDYKKQCODAT---SVSGIGADTVWNSLGYDGSGVVVALVDTGID 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 AX------VEEDHYAJALAQFYPYGIPLIKADKV-QAGGFKGAHYKVAVLDFGIQ 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 ANHPOLKGKVIGHTDAVNSRDEPYDDQGHGTHVAGIVAGTGSVNSOYIGVAPGAKLVGVX 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 ASHPDL - NVVGASFVACENINTDGNGHCTHVACTVAALDNTTG-VLGVAPSVSLYAVK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 VLGADGSGSVSTIIAGVDWVVQNKDKYGIRVINLSLGSSQSSDGTDSLSQAVNNAWDAGI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 VVCVAAGNSGP--NTYTVGSPAAASKVITVGAVOSHDNIASPSSRGPTADGRLKPEVVAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IS2 VYVAAAGNSGSSGNTNTIGETATEDSVIAVGAVBANGNRASFSSVG-----AELEVAAAP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 GVDIIAPRASGISMGTPINDYTIKASGISMATPHYSGYGALILQAHPSWTPDKYKTALIE 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MULTIMESTRATES THE PROPERTY OF THE PROPERTY OF
                                                                                                                                                               0.-NOV-1996 (FERMELTEL. ): Created)
01-NOV-1996 (FERMELTEL. (1) Last Sequence update)
01-DEC-2001 (FERMELTEL. A). Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TERMELCE) .5. treated)
01-MAR-2001 (TERMELCE) .5. treated)
01-MER-2001 (TERMELCE) .5. that sequence update)
01-DEC-3001 (TERMELCE) .59. det candotation update)
SOBTILISIN PRECUNSOR (EC.) 3.4 21.62) (FRAGRET)
                                                                                                                                                                                                                                                                                                                                                                                         Bacteria: Firmicutes; Becillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_FaxID-1402;
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                                                                                   PRELIMINARY;
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Bacillus licheniformis.
                                                                                            053521
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                RESULT 12
053521
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09F941
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PRILINE-STRAIN-EIUS 815.
PROLINE-STRAIN-EIUS 815.
PROMIN K.L., Croder J.S., Willer F.S.;
Subtilliains of Sacullus spp. Nydrolyse keratin and allow growth, og.)
308 GVYSTYPTHTYAT-LNGTSMASPHVAGAAALILSKHPNLSASOVRNRLSSTATYLG----353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.1 Sovre 56.15, DB 2; Length 374; Best Local SILILILE 119. 39.00 M. Pred No. 1.18-72; Indels 49: Capt Matches 149; Conservative 54; Mismatches 130; Indels 49: Capt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 GYFGNTRVSGIKFIQEDYXVQVDDAT---SV8QIGADTVHNSLGYDGSGVVVALVDTG1D-17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 ANHPOLKGKVIGWYDAVNGRSTPYDDQGHGTHVAGIVAGIGSVNSOYIGVAPGAKLVGVK: 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 VVCVAAGNSCP--NTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAP 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 AY------VEEDHVAHALAQTVPYGIPLIKADKV-QAGGFKGANVKVAVLDTGIQ1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 ASHPOL--NVVGGASFVAGEAYNTDGACHGFHVAGTVAALDHTTG-VLGVAPSVSLYAVK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 VLGADGSGSVSTIIAGVDATVQNKDKYGIRVINLSLGSSQSSDGTDSLSGAVNNAMDAGI 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 GVDIIAPRASGTSNGTPINDYYTKASGTSMATPHVSGVGALILQABPSWTPDKVKTALIE 409
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01-WAR-2001 (TrENBLED). 16, Lest sequence update)
01-08C-2001 (TrENBLEB). 19, Last annotation update)
SUBILLISIN PRECURSDR (EC 3.4.21.62) (FRAGNERT).
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                                                                                                                     Pair F.M. Chan S.T., Olico S.B.;

Pair F.M. Chan S.T., Olico S.B.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.24; Score 556.5; DB 2; Length 379; 38.4%; Pred. No. 2.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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01-NOV-1996 (TERMILEL) G. Liat sequence update)
01-NOV-2001 (TERMILEL) 19. Liat ennotation update)
SUBSTILISIN GARLSBERG PREUNSQR.
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Bacillus/Staphylococcus group: Bacillus
NCBI_FaxID-1402;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 AA
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TALESPO. IPROGRADE, PERLIADS.

PERM. PROGRAD, SURTILISEN.

PROSTER, PROGRAT, SURTILISEN.

PROSTER, PROGRAT, SURTILISEN.

PROSTER, PROGRAT, SURTILISEN.

PROSTER, PROGRAM, SURTILISEN.
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                             Query Match 16.2N; Score $58.5; DB 2; Length 374; Case State 25 Length 374; Matches 157; Conservative 60; Manaches 137; Indels 81; Gaps 17; Matches 157; Conservative 60; Manaches 137; Indels 81; Gaps 17; Case 176; Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 VSGIKFIQEDYKVQVDDAT --- SVSQIGADTVWNSLGYDGSGVVVAIVDTGIDANHPULK 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 IMPGSYGDRDRAVK --VLRLMGAQVKYSYKIIPAVAVKIKARDLLLIAGMIDTGYFGNTR 1,2,1
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                                                                                                                                                                                                                                                                                                                                                                                                                         and another, the page 1. Alter E S.; Aller E S.; Aller
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374 374 374 6401422813D0E60 CRC64;
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01.W07-1996 (TrEMBiral, 01, Last Sequence update)
01.DEC-2001 (TrEMBirel, 19, Last annotation update)
SUBSTILISIN ONLASEERS PRECURSOR.
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Bectrie: Pirmicutes; Bacillus/Clostridium group;
Bacillus/Stephylococcus group; Bacillus.
Bacterla: Firmicutes; Bacillus/Clostridium group;
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10517 GALCARGACCTCTACACTTACCTCTACCTCTACACTACAACTTCTACAT 10458 11222 GCTGGCAGAGCAAGTGGAAGCATGGGTCAACCAATTAATGACTATTACACGCAGCT 11163 11162 CCTGGGACATCGCAACTCCTCACGTAGTGGAGCCCCTCTTCCTCACCA 11103 11102 CACCCGAGCTGGACTCCGGACAAGTAAAAACAGCCCTCATAGAAACTGGTGATATCGTA 11043 L1042 AAGCGAGATGAAATAGCGGATATAGCCTACGGTGCAGGTAGGGTTAATGCATACAAGGCT 10983 10982 ATAANCTAGGATAACTATGCAAAGCTAGTGTTCACTGGATATGTTGCCAACAAAGGCAGC 10923 10863 10802 TCTTACACCCCTACTATGGATTCGATAGGTGGTTATTACANCCCAACTGATGGAACA 10743 10742 TGGACANTTAAGGTTGTAAGCTACAGGGGAAGTGCAAACTATCAAGTAGATGTGGTAAGT 10683 10682 GATGGTTCCCTTTCACAGCCTGGAAG------TTCACCATCTCCACAACCA 10638 10577 GACACCTITACAATGACGGTAAACTCTGGGGCTACAAAGATTACTGGAGACCTAGTGTT 10518 10457 AGATCGGAGAGTTCCAACAGCFACGAACAGGTAGAATACTTAAACCCGGCCCAGGAACC 10398 10397 TGGTACTTCCTAGTATASCCTACTACCTTACGGTTGGGCTTACTACGAGCTGACGCT 10338 1543 TGGACGGTCAAGGTCGTCAGCTACAAGGCCGGCGAACTACCAGGTCGACGTCGACGTCGCGC 1602 1063 GCCCGCGCCCCAGCGGAACCAGCATGGCACCCCGATAAACGACTACTACACCAAGGCC 1122 1243 GCCCCCAAGGAGATAGCGGACATCGCCTACGGTGCGGGTAGGGTGAACGTCTACAAGGCC 1302 1563 ACCCCCACCACCCACACCCAGACCTTCACCGGTTCCCTTAACGACTACTGGGACACCAGC 1722 1723 GACACCTTCACCATGAACGTCAACAGGGGTGCCACCAAGATAACCGGTGACCTGACCTTC 1782 1903 TGGACGTTCCTCGTCTACGCCTACAGGACGTACGGCTGGGCGGACTACCAGCTCAAGGCC 1962 1363 GCCACCCACACCTTCGACGTCAGGGGGGCCACCTTCGTGACCGCCACCCTCTACTGGGAC 1483 TCCTACACCGCCTACTACGGCTTCGAGAAGGTCGGCTACTACAACCCGACCGCCGGAAGC 1123 TCTGGAACCAGCATGGCTACCCGCACGTTTCGGGCGTTGGCGGCGTCATCCTCCAGGCC 1183 CACCCGAGCTGGACCCCGGACAAGGTGAAGACCGCCTCATCGAGACCGCCGACATAGTC 1303 ATCAMGTACGACCACTACGCCAAGCTCACCTTCACCGGCTCCGTCGCCGACAAGGGAAGC 1603 GACGGGAGCCTCAGCCAGTCCGGCGGCGAACCCGAATCCAAACCCCAACCCGAACCC 11near DNA 1962 bp (Sequence 15 from patent US 6358726, AR201155 AR201155.1 GI:20252043 10337 AAAGTTTATTATGG 10324 1963 GTCGTCTACTACGG 1976 DEFINITION ACCESSION VERSION KEYWORDS SOURCE RESULT 4 AR201155 5000 g g g à a g g à 合 ò S à g à 셙 à 용 à 용 à 8 à 용 à à à ò à à

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1712 GGGACACCACGACACCTICACATANACGTCAACAGCGGTSCCACCAAGATAACGGTG 1771
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                                                     992 TOTOCOAGCAGGGACCGMICOCOGNOGOAAGGCTCAAGCCGGAAGTCGTCGCCCGGCG 1051
                                                                       992 TCTCAAGCAGAGGGCCAACTGCAGGGAGGCTTAAGCCTGAGGTTGTTGTTGCTCCAGGAA 1051
                                                                                                                                      1052 TIGACATCATAGCCCCGCGCGCCAGCAGCAACCAGCATGGCACCCCGATAAACGACTACT 1111
                                                                                                                                                                 1112 ACACCAAGGCCTCTGGAAGCAGCATGGCCACCCCGCACGTTTCGGCGCTTGGCGCGCTCA 1171
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932 CAGCTGCAAGCAAACTTATTAGAGCCGTTGACAAGTATGATATAACAAGCT 991
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                                                                                                                                                                                                                                                                                                                     110 AGNAGANCTACGGACTGCTGACCCCGGGGACTGTTCAAGAAAGTCCAGAGGATGAACTGGA 169
                                                                                                                                                                                                                                                                                                                                                                  107 AGANGAACTATOOTCTGCTAACGCCAGGACTGTTCAAAAATTCAAAAATTGAATCCTA 166
                                                                                                                                                                                                                                                                                                                                                                                                                   170 ACCAGGNAGTGGACACGTCATAATGTTCGGGAGCTACGGAGACAGGGACAGGGCGGTTA'229
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0; Mismatches 618;
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NGACAAAGTAAAAAGAGGCCTCATAGAAACTGCTGA 839

PAT 04-DEC-1998

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Horishita, H., Asada, K., Tsunasava, S. and

CTCGGCGTCAAGGTTCTCGGTGCCGACGCTTCGGGA 717 GF7GACTGGGTCGTCCAGAACAAGGACAAGTACGGG 777 GTTGACTGGGTCGTCCACAACAAGGATAAGTACGGG 183 GGCTCCTCCAGAGCTCCGAGGAACCGACTCCCTC 837 GACGGCGGTATAGTAGTCTGCGTCGCCGCCGCCAAC 897

Score 512.8; DB 6: Length 564; Pred. No. 9.2e-58; ; Mismatches 17; Indels 0: Gaps GTTGCCGGAACCGCCAGCGTTAACTCCCAGTACATA 657 GTTGCCGGAACAGGCAGCGTTAACTCCCAGTACATA 63

CGACCTCTACCTCTACGACCCCAACGGGAACGAGGT 1475 CGCCTTCGAGAGGTCGGCTACTACAACCCGACCGC 1535

In codons is given for each COS. Hereilly the highest scoring match found by fasts -0 is given for	Construction of possible ribonary observations of the detables. The position of possible ribonary butting site sequences are strengther than the position of possible ribonary butting site sequences are strengther than the position of the	Acids Research, 22/23,4758-4778(1994); and the FramePlot program of Sibb et al., Gene 30:157-66 (1994) as implemented at the http://www.inla.go.jp/ (1904) as implemented at a single-sibility of the control of the con	correct initiations officen, where possible we choose an initiation code (table initiation) equal (up or (ett)) which is preceded by an upstream cribaneme brinding after sequence (ob)Lailly 1-31bp before the initiation coden) if if this cannot be identified we choose the nost	upstream intilation codo. INFORTANT THIS SEQUENCE MAY NOT be the entire insert of the sequence continued to the sequence continued obtains. It is any be shorter because we only sequence overliapping sections once, or longer, because we atranse for a continued sections once, or longer,	anali Overige beveen respicanting speniations. Consid 51A Overlaps count of 75 on the Assi 79 spenia restriction fragment. FRAUMES COUNT OF STANDING STANDIN	(Partial - All) (Partial - All) (Partial - All) (Partial - All) (Control - Control - Control (Control (Control	Agene-1927A.010, putchive membrase transport protein. // none-1927A.010, putchive membrase transport protein. // none-1927A.010, putchive membrase solitobio: // none-1927A.010, putchire putchire solitobio: // none-1927A.010, putchire putchire societo ont. 20 // none-1927A.010, putchire	fasts sporces opt. 1021 - seocer 10403.4 (F): 0 4 0.0.64 identity in 773 as overlap and TR:068022 (BML: ALOSIUS) SCHY, 105 (G) as p. fasts sporces por; 163 a. sporces 165.0 E(p): 1.4e*5,3.37.34 identity in 764 as overlap. Opticals	nullipp possible transmembrane hydrophobic dosains. //odoin_start=1 //cromit_bable=1: bable=1: bable=1: procession for the proc	/ Ap. zee = 'creptory's - 'cre	A VEGGORANDERNO ELEGE ELON ANTICALES DE ANTI	VONSQUEGATE AND	RBS AGAINT WAS ANY FOR LONDON ANA RBS A423. 1823 gent A7416-1824 FAST AND A7416-1824 FAST A741	CDS 7332. 2792	/trans_table=1. /product="hypothetical protein SCF51A.02.
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Best Local Similarity 54.8%; Pred. No. 1.5e-22;
Matches 659; Conservative, 0; Mismatches 508;
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1318 TACGCCAAGCTCACCTTC/ACGCGCTCGCTCGCCAAAGGGAAGCGCACCACACCTTC 1377

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1498 TACGGCTTGGAGAAGGTCGGCTACTACAAGCCGAACCGGGAACCTGGAGGGTCAAGGTC_A557 ò

ð a 1618 CAG 1620

Db 11091 CTG 11093

linear AR202321 2809 bp DNA Sequence 1 from patent US 6361987. AR202321 AR202321.1 GI:20256860 LOCUS DEFINITION ACCESSION RESULT 8 AR202321 VERSION

Unknown. Unclassified. Unknown. SOURCE REFERENCE

Gene encoding a procein having asymmetric hydrolase activity for a sankettuted 1.4-dihydropyridine derivatives and its expression product us 6361987.A 1.56-WAR-2002; 1 (Dases I to 2809) Ariaeve, A. Maraufuji, M. Tsuruta, T., Dobashi, K., Nakashima, T., Isshixi, K. and Yoshioka, T. 311 t /organism-"unknown" 1041 c 984 g Acation/Qualifiers 2809 source JOURNAL PEATURES AUTHORS TITLE

Query Match
Bast Local Saminarity 54.34, Pred No. 3:e-73, Indels 48; Gap?, Astches 93; Conservative O; Mismatches 439; Indels 48; Gap?.

BASE COUNT

332 TGATAGACACGCGTACTTCGCTACACACACGCGTCTCGGGGCATAAAGTTCATACAGGAGG 391 392 ATTACAAGGTTCAGGTTGACGACGCCACTTCCGTCTCCCAGATAGGGGCCGATACGGTCT, 451 930 ACGGGGTCCGCAGGGCCCCCTCGACACTCCGTCGGGCAGATCGGCGCCCCCAAGGCGTT.893 S à

452 GGAACTCCCTCGGCTACGACGGAAGCGGTGTGGCTTGCCATCGTCGATACGGGTAYAG \$11 ò g

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512 AGGGANGCACCCGATCTGAAGGGAAGGTGATAGGCTGGTACGACGCGTCAAGGGC 571 572 GGTCGACCCCTACGATGACCAGGGACACGGAACCCACGTTGCGGGTATCGTTGCOGGAA 5\$1 윱 윱 ò ò

CCGGCAGC---GTTAACTCCCAGTACATAGGCGTCGCCCCGGGCGCGGGGCGCGTCGTCGGGG '538

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Page 10

1284 GGG-------CGGCCCCCCAGGCCCCCACCTCCTCAACATGAGCCTGGGCGGCA 1331 749 GGGTCGTCCAGAACAAGACAAGACAAGGGATAAGGGTCATCAACCTCTCCCTCGGCTCCT 808 e å

989 GCTTCTCCAGCAGCGACCGAC---CGCGGACGGAAGCCTCAAGCGGAAGTCGTCGCCCC 1045

PAT 20-APR-2002

1217 CCCTCATCGAGGGGGGGGACATAGTCGCCCCCAAGGAGATAGCGGACATCGCCTACGGTG 1276 1277 CGGGTAGGGTGAACGTCTACAAGGCCATCAACTACGACGACGACGAAGGTCACGTTCA 1336 1686 GCGCGGCGCCCCCCCCGAACAACACCCCCACTGGACCCCCCCAACAACGGCC 1745 1746 correspondenceasons and assessing 1796

1337 CCGGCTCCGTCGCCGACAAGGGAAGCGCACACACACACATCGAACGTCAGC 1386
1357 TGAAGTTCGGCGTCCAGAAGTGCCGCCAAAACGAAGAAGAAGCGATCGGGTCCC 1908 ≳

Streptonyea viridespotus dipp DRA linear BCT 07-3HN-2002 Streptonyea viridespotus dipp yene for 1.4-dhydropyridise esmanitospective de-grass, complete cds. AB007809.1 GI:Z:322743

DEFINITION

COCUS

KEYWORDS

VERSION

ABOO7809 ACCESSION Streptomyces virilosoporus (strain:4-914) DNA. Streptomyces virilosporus Streptomyces virilosporus, Actinobacterides, Actinomycesiaes; Streptomycinese; Streptomyces-Actinomycesiaes; Streptomycinese; Streptomyces-SOURCE REFERENCE

Arigowa, A., Matsufiji, M., Nakashima, T., Dobashi, K., Tsshixi, K., Yoshikof, T., Yanasha, F., Manosel, H. and Taylothi, S. Stroptonyces Serling Protease (DHP-A) as a New Biocrealyst Capable of Poraing Chical Intermediates of 1,4-Dihydropyridine Calcium Appl. Environ. Microbiol. 68 (6), 2716-2725 (2002) 22034940 12039725 AUTHORS

TITLE

2 (bases 1 to 3900) JOURNAL MEDLINE PUBMED REFERENCE

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VCA429230 3030 bp mRNA linear pth 03-JUN-2002 VCA429230 CONTROL (. hegariensis mRNA for pherophorin-dzi protein. A4459230
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Arigano, Astaviji, M. Teurute, T., Dobashi, K., Nokashima, T., Jashiki, K. and Yoshioka, T. Lashiki, K. and Yashii, M. A. Jashii, M. Jashii, M. A. 
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When "SCC21 DDC.

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Bluding-Portain-dependent transport aystems inner membrane
component, score 81.20, E-value 2.2e-20*
complement(1037, .3123)
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tinner membrane comp sign.
Anner membrane (360). 4571)
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/product=putstye sugar transporter membrane protein*
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- 1158 CGTTGCCCCCTCATCCTCCAGCCCCACCCGAGCTGGACCCCGGACAAGGTGAAGACCGC71217
 - 21016 GGCGGCCGCTCTGCGCGCGCGCGCGGCGCCCTCAGCGCCCCTGAAGAACGTC729957
 - 20956 CTCGCCAGCAGTTCGCA-----CCCCACTCCGCGGTACGACGCGTTCCAGGCCGCAG 1218 CCTCNTCGAGAGGGGGGACATAGTGGCCCCCAAGGAGATAGCGGACATCGCCTACGGTGG g
- 1278 GOGTAGGGTGAACGTCTACAAGGCCATCAAACTACGACGACGACGACGCCAAGCTCACCTCACCTTCACTTCACTTCACTTCACCTTCACCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT g
 - 1338 CGGCTCCGTCGCCGACAAGGGAAGCCCACCCACCCTTCGACGTCAGCGGCGCCCCCTT 1397
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                                                     1861 AGCTACGAGGCACGTCGAGTACGCCAACCCGGGGGAACCTGGAGCGTTCCTCGTCGACCTGACCACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTTCCTCCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTTCACCTCGACCTTCCTCCTCCTACCTCGACCTTCACCTCGACCTTCACCTCGACCTTCACCTCGACCTTCACCTCGACCTTCACCTCGACCTTCACCTCGACCTTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCT
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Pred. No. 2.2e-263;
0; Mismatches 292; Indels 9; Gaps
                                                                                                                                                                         1921 GCCTACAGCACCTACGGCTGGGCGGACTACCAGCTCAAGGCCGTCGTCTACTACGGG 1977
                                                                                                                                                                                                                                                 1921 GCCIACAGCACCIACGGCIGGGCGGACTACCAGCTCAAGGCCGTCGTCTACTACGGG 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TSUNASAWA, Sugumu
APPLICANT: KATO, IKUNOGO, IKUNGA
APPLICANT: KATO, IKUNGAMBANOSTABLE PROTEASE GBMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINATYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pertentin Release #1:0, Version #1.30
CONRENT APPLICATION DATA:
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FILING DATE. 20 AM. 1998
CLASSITCATION LATA.
APPLICATION LATA.
APPLICATION NUMBER PCT/1996/03253
FILING DATE. 07-N0V-1996
FRICOR APPLICATION DARRA:
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FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08894818B
Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TAKAKURA, Hikaru
APPLICANT: WORISHITA, Mio
APPLICANT: YAMAMOTO, Kateuhiko
APPLICANT: MITTA, Masanori
APPLICANT: ASADA, Kiyozo
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TELEFAX: (202) 737-5528
INPORATION FOR SED ID NO: 6: SEQUENCE CNARACTERISTICS:
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Best Local Similarity 83.9%;
Matches 1573; Conservative
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REGISTRATION NUMBER: 2
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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APPLICANT: TARAKU:
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11.24 CTGGAACCAGCAGCCAGCCACCCTTTCGGGCGTTTGGGCGCGCTCATCCTCCAGGCCC 1183 1184 ACCGAGCTGGACCCCGGACAAGGTCAAGACGCCCTCATCGAGACCGCCGAAAGTCG 1243 944 AGGICATAACCGICGGTGCAGFTGACAGCAACGACAICGCCCAGCTICTCCAGCAGGAGG 1003 1004 GACCGACCGCGGACGGAAGGCTV.AAGCCGGAAGTCGTCGCCCCGGCCGTTGACATCATAG 1063 1064 CCCCGCGCGCCAGCGGAACCAGGATGGCCACCCGATAAACGACTACTACAACGACT 1123 1124 CTGGAACCAGCATGGCCACCCCCCCACGTTTCGGGGGTTGGCGGCGCTCATCCTCCAGGCCC 1183 1184 ACCCGAGCTGGACCCCGGACAAGGTGAAGACCGCCCTCATCGAGACCGCGCGACATAGTCG 1243 230 AGGTACTGAGGCTCATGGGGGGCUCAGGTCAAGTACTCCTACAAGATAATCCCTGCTGTGT 289 227 GAGTICITGAGITAATGGGGGGGCAAAAGTIAGGGATGTGTACCAATATATACCCGCAATAG 286 290 CGGTTAAAATAAAGGCCAGGGACCTTCTGCTGATCGCGGCATGATA---GACACGGGTT 346 287 CIGCCGATCTTAAGGTTAGAGACTTACTAGTCATCTCAGGTTTAACAGGGGGTAAAGCTA 346 347 ACTTCGGTAACACAAGGGGCGCGCATAAAGTTCATACAGGAGGATTACAAGGTTCAGG 406 347 AGCTTTCAGGTGTTAGGTTTATCCAGGAAGACTACAAGTTACAGTTTCAGCAGAATTAG 406 107 TIGACGACGCCACITCCGTCTTTCAATAGGGCCGATACCGTCTGGAACTCCCTCGGCT 466 407 AAGANTEGATGATGAGTCTGCAGGTCAAGTTATGGCAACTTACGTTTGGAACT---TGGGAT 463 467 ACGACGGAAGCGGTGTGGTTGCCATCGTCGATACGGGTATAGACGCGAACCACCCG 526 464 ATCAIGGTICTGGAATCACAATAGGAATAATTGACACTGGAATYGACGCTTCTCATCCAG 523 527 ATCTSAAGGGCAAGGTCATASGCTGGTACGACGCGGGTCAACGGCAGGTCGACCCCTACG 586 587 ATGACCAGGGACACGAACCCACGTGCGGGTATCGTTGCCGGAACGGCAGCG---TTA 643 584 ATGACCATGGACATGGACTCATGTAGCTTCAATAGCAGGTGGTACTGGAGCAGGAAGTA 643 644 ACTCCCAGTACATAGGCGTCGCCCCGGCGCGAAGCTCGTCGGCGTCAAGGTTCTCGGTG 703 644 ATGGCAAGTACAAGGGAATGGCTCCAGGAGCTAAGCTGGCGGGAATTAAGGTTCTAGGTG 703 763 04 CCGAIGGITCIGGAAGCAIATCIACIAIAAITAAGGGAGIIGAGIGGGCCGIIGAIAACA 763 764 AGGACAAGTACGGGATAACGGTC4TCAACCTCTCCCTCGGCTCCTCCCAGAGCTCCGACG 823 824 GAACCGACTCCTCAGTCAGCCGTCAACAACGCTGGGACGCCGGTATAGTAGTCTGCG 883 824 GAACCGACTCCCTCAGTCAGGCCGTCAACAACGCCTGGGACGCCGGTATAGTAGTAGTCTGCG 883 884 TCGCCGCCGGCAACAGCGGGCCCGAACACCTACACGGTCGGCTCACCGGCGGCGCGGGGCA 943 884 TOGOGGOGGOAACAGOGGGCGAACACTACACGTGGGTGACCGCGCGCGCGCGAGGA 943 704 CCGACGGTTCGGGAAGCGTCTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACA

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Librity 100.04; Pred. No. 2.8e-224;
Conservative 0; Mismatches 0; Indels
              SYSTEM: FC-DOS/MS-DOS
Patentin Release 11.0, Version 41.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAKAKURA-1
              OPERATION SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PALENCIA RELEGGE 11.0, VC
CURRENT APPLICATION DATA: A00/894,818B
FILING DATE: 20-WAY-2938
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRICK APPLICATION DATA:
PRELICATION WINNER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 323285/1995
FILING DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTOMOTOR TO STATE OF THE STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: genomic DAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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Matches 1165; Conserva
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1364 CONCCACACCTTCGACGTCAGCGGGCCCACCTTCGTGACGGCCACCTCTACTGGGACA 1423.
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STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
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: Sequence 1: Appllcation US/088948188

: Patent No. 6261822

: GENERAL INPORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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413 CTACTGGGACACGGGCTCGAGTGACATCGACCTCTACCTCTACGACCCCAACGGAACGA 1472



STATE: D.C. 20004 : TIP:

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1066 COGCGOGCAGCGGAACCAGCAGCACCCCGATAAACGACTACTACAACCAAGGCTCT 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 GATGACCAGGGACCGGAACCCACGTTGCGGGTATGCTGCAGCGGAACCGGAACCGGAACCGGAACCGTAAAC 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GACAAGTACGGGATAAGGGTCATCAACCTCTCCCTCGGCTCCTCCCAGAGCTCCGACGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 ACCARCTCCCTCAGTCAACCCCTCAACAACACCCCCGGTATAGTAACTCTGCCTC 360
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Pred. No. 4.4e-158;
0; Mismatches 24; Indels
MBER: JP 1994/130236
13-JUN-1994
                                                                                               JP 1994/173912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.14/
                                                          PRIOR APPLICATION DATA. 3P 19
APPLICATION NUMBER: JP 19
FILHS DATE: 26-JUL-1994
ATTORNEY.AGENT INFORMATION:
NAME: BROMDY, ROGEL.
REGISTRATION NUMBER: 25,6
                                                                                                                            26-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natches 874; Conservative
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TELEFAX: (202) 737-352
INFORMATION FOR SEG ID NC:
SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 898 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                       REPERBNCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORM
TELEPHONE: (202) 628-
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-750-532-7
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                                                                                                                                                                                                                                                                                                                                                                                                           1653 CCCGAACCCAACCCGGACCACGGACACCCAGACCTTCACCGGTTCCGTTAACGACTACTG 1712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1021 CCTCGTTGACAGGTCGAGGAGGAACAGGTAAGGAGGAGGAGGTAGGAGTAGGCGCAACCGGG 1030
                                                                                               1473 GGTTGACTACTCCTACACCGCCTACAGGCTTCGAGAAGGTCGGCTACTACAACCCGAC 1532
                                                                                                                                                                                                                                  1533 GGCGGGAACCTGGACGGTCAAGGTCGTCAGCTACAAGGCGGGGGGGAACTACCAGGTCGA 11592
                                                                                                                                                                                                                                                                                                                                                                      1593 CGTCGTCAGCGACGGGAGCTCAGCCAGTCCGGCGGCAACCCGAATCCAAACCCAA 1852
                                                                                                                                                                                                                                                                       1893 COCGGGAACTGGACGTTCCTCGTCTACGCTACAGCACTACGGCTGGGCGGACAAAA
601 CTACTGGGACACGGGCTCGAGCGACCTCTACCTCTACGAGCGCCCAACGGAACGA 869
                                                                                                                                   1081 CCCGGGAACCTGGACGTCCTCGTCTACGCCTACAGACCTACGGCTACGGGC
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TREET: 419 Seventh Street N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION MNBRR: PCT/JP95/01095
FILLING DATE: 05-JTH: 1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08750532
Patent No. 5756339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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MEDIUM TYPE: Floppy
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US-08-750-532-7
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1246 CCCAAGGAGATAGCGGACATCGCCTACGGTGCGGGTAGGGTGAAGGTCTACAAGGCCATC 1305
                                             720 CCCAAGGAGATAGGGGACATCGCCTACGGTGGGGTAAGGTCAACGTCTTCAAGGGCATC 779
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PAPICONT MANOTO KRASHINO
PAPICONT MANOTO KRASHINO
PAPICONT KINA MASSOCIA
PAPICONT TSUNGAM, SUBBOOT
PAPICONT TSUNGAM, SUBBOOTONIS GENES
TITLE OF INVESTION: HIRTONISMINE PROTENSE GENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Browdy and Neimark
419 Seventh Street N.N., Ste. 300
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FILING DATE: 20-HAY-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/088948188
Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
WIDTUM TYPE: FORPPY LISK
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anomic DNA
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
US-08-894-8188-17
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Query Match
40.8%; Score 806.8; DB 4; Length 1464
Best Local Similarity 99.1% Pered No. 8-95153; Anches 81; Conservative 0; Mismatches 16.7; Indeas 0.6ap 0.
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TITLE OF INVENTION: HYPENTHERMOSTABLE PROTEASE GENES NUMBER OF SECUENCES: 82

CORRESPONDENCE ADDRESS ADDRESSEE: Browdy a

GGAACCCACGTTGCGGGTATC3TTGCCGGAACCGGCACGTTAACTCCCAGTACATAGGC 660 1367 GICTOCACCATCATCGCGGGTGTTGACTGGAACGTCCAGAACTAGGACAAGTACGGGATA 1426 886 241 CTCATGGGCGCCCAGGTCAGTACTCCTACAAGATAATCCCTGCTGTGGCGGTTAAAATA 300 301 AAGGCCAGGGACCTTCTCCTGATCGCGGCCATGATAGACACGGGTTACTTCGGTAACACA 360 361 AGGGTCTGGGCCATAAACTTCATACAGGAGGATTACAAGGTTCAGGTTGAGGACGCCACT 420 421 TCCGTCTCCCAGATAGGGCCGATACCGTCTGGAACTCCCTCGGCTACGACGGAAGCGGT 480 481 GTGGTGGTTGCCATCGTCGA*ACGGGTATAGACGCGAACCACCCCGATCTGAAGGGCAAG 540 GECTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGGACAAGTACGGGATA 780 61 GCCCTTGCGGCACCCGTAAAACCGGTTGTCAGGAACAACGCGGTTCAGCAGAACAACTAC 120 181 GACACCGTCATAATGTTCGGGAGCTACGGAGACAGGGACAGGGCGGTTAAGGTACTGAGG 240 1 ATGAAGAGGTTAGGTGCTGTGCTGGCACTGGTGCTCGTGGGTCT7CTGGCCGGAACG 1427 AGGSCATCAACCTCTCCCTCGGCTCCTCCCAGAGCTC 1464 781 AGGGTCATCAACCTCTCGCTCGCTCCTCCCAGAGCTC 818 Sequence 34, Application US/08894818B Patent No. 6261822 GENERAL INFORMATION: APPLICANT: TSUNASAWA, SUSLETU APPLICANT: KATO, IKUNOSħLD US-08-894-818D-34 601 8

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37.9%, Score 750.2, DB 4, Length 1962,
64.7%, Pred. No. 1.9e-141,
iive 0, Mismatches 618, Indela 48, Gapa. 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 ACCAGGNAGTGGNCACCCTCATAATGTTCGGGNGCTACCCACACAGGGACAGGGCGGTTA 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 -----GACGACGCGACTTCCGTCTCCCAGNTAGGGGCCGATACCGTCTGGA 454
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COMMUTER: IMM PC COMPATIBLE
OPERATUR SYZED: CP.056/45-006
SOCTAME: Retent.n Release 11.0, Version 11.30
CORRENT PROLICATION DAYA
PRILICATION NAMER: US/08/594,6188
FILING DATE: 20-004/1998
419 Seventh Street N.W., Ste. 300
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APPLICATION NUMBER: PCT/JP96/03253
PILING DATE: 07-NOV-1996
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APPLICATION NOWBER: 19 33285/1995
PILLED DATE: 12-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Broady Roger, 78,618
REDIESTRATION WINDER: 25,618
                                                                                                                               United States of America
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Matches 1219; Conservative
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                                       Washington
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                                                                                                                               COUNTRY:
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1637 CTCCACAACCAGAACCAACAGTAGACGCAAAGACGTTCCAAGGATCCGATCACTACTACT 1696
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Sequence 13. Application 05/0444517

Figure 14. Application 05/0444517

Figure 14. Application 05/0444517

Figure 14. Application 05/0444517

Figure 14. Application 05/044417

Figure 14. Application 05/04/14,172

CORRECT PARTICUPE 12. APPLICATION 05/04/14,172

CORRECT PARTICUPE 12. APPLICATION 05/04/14,172

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Figure 14. Application 05/04/14,172

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107 AGANGAACTATGGTCTGCTAACGCCAGGACTGTTCAAAAATTCAAAATTGAATCCTA 186 170 ACCAGGANGTGGACACCGTCATAATGTTCGGGAGCTACGGAGACAGGGACAGGGCGGTTA 229 67 ACGAGGAAATCAQCACAGTAATTGAAAACCATAGGGAAAAGAAATTGCAGTAA 226 230 AGCTACTGAGGCTCATGGGCGCCCGAGGTCAGTACTCCTACAAGATAATCCCTGCTGTCG 289 127 GAGTTCTTGAGTTAATGGGTGCAAAAGTTAGGTATGTGTACCATATTATACCGCAAAAG 286 290 CGGTTAAATAAAGCCAGGGACCTTCTGCTGATCGCGGGCATGATAGACACGGGTTACT 349 110 AGAAGAACTACGGACTGCTGACCCGGGACTGTTCAAGAAAGTCCAGAGGATGAACTGGA 169 187 CTGCCGATCTTAAGGTTAGGAGCTTACTAGTCATCTCAGGTTTAACAG-------334 37.9%; Score 750.2; DB 4; Length 1962; 64.7%; Pred. No. 1.96-141; tive 0; Mismatches 618; Indels 48; Gaps Ouery Match Best Local Similarity 64.7% Matches 1219; Conservative 윱 å g 윱 a ò ð à

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1116 CAAGGCCTCTGGAACCAGCAAGCAACCACCGCACGTTTCGGGCGTTGGCGCGCTCATCCT 1175
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NAME: BICHOY, ROSE L. 5.19
RETERRICHOUSER: 25.519
RETERRICHOUS NEW RESET TANK
TELEBRONE: (202) 639-516;
TELEBRONE: (202) 639-516;
SENDERY: (202) 639-5
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STRANDEDNESS: double
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TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
WINNER OF SEQUENCES: 42
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CURRENT APPLICATION DATA:
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ADDRESSE: Broady and Neimark
STREET: 419 Seventh Street N.H., Ste. 300
CITY: Neahington
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FILING DATE: 20-MAY-1998
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APPLICATION NUMBER: PCT/JP96/03253
FILING DATE: 07-NOV-1996
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PRIOR APPLICATION WORDER: JP 323285/1995
FILING DATE: 12-DEC-1995
ATTORIEY/ACENT INPORMATION:
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COUNTRY: United States of America
ZIP: 20004
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COMPUTER: ISM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent NO. 6261822
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 CTTGGGATATGATGGTLCTGGAATCACAATAGGAATAATTGACACTGGAATTGACGCTTC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 CCACCCCGATCTGAAGGGCAÄGGTCATAGGCTGGTACGACGCCGTCAACGGCAGGTCGAC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 TCATCCAGATCTCCAAGGAAAAAATGGGTGGGTAGATTTTGTCAATGGTAGGTTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          579 CCCCTNCGATGACCAGGGACACGGAACACGTTGCGGGTATCGTTGCGGGAACGGGCAG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 TCCATACGATGACCATGGACATGGACCTCATGACCTCCATAGCAGCTGGTACTGGAGC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639 CG---TTAACTCCCAGTACATAGQUGTCGCCCCCGGCGCAAAGCTCGGCGTCAAAGT 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            596 TCTCGGTGCCGACGGTTCGCCAAGCGTCTCCACCATCATCGCGGGTGTTGACTGGGTCGT 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              816 CTCCGACGGAACCGACTCCCTCAGTCAGGCCGTCAACAGGCCTGGGACGCCGGTATAGT 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459 CCTCGGCTACGACGGAAGCGGTGTGGTGGTTGCCATCGTCGATACGGGTATAGACGCGAA 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
15.04; Score 692.8; DB 4; Length 1566;
Best Local Similarity 67.14; Pred. No. 5.3e.130
Matches 1020; Conservative 7.0; Missarches 483; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: /note- N at position 1283 is G or T
TAKAKURA-1
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Page 11
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Score 560.4; DB 4; Length 1236; Pred. No. 1.4e-103; 0; Mismatches 371; Indels 3; Gaps

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396 CAGCAGGGGACCGACCGCAACGGAAGGCTCAAGCCGGAAGTCGTCGCCCCGGGGGTTCA 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .116 CAAGGCCPCTGGAACCAGCAAGGCACCACCGGCACGTTTGGGGGGTTGGCGGCGCTCATCCT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1236 CATAGTCGCCCCAAGGAGATAGCGGACATCGCCTACGGTGCGGGTAGGGTGAACGTCTA 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1296 CAAGGCCATCAAGTACGACGACTACGCCAAGCTCACCGGCTCACCGGTCGCTGGCGGAA 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ACCAAGTAATGGCAAGTACAAAGGGAATGGCTCCAGGAGGTAAGGT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 TCTAGGTGCCCATGCTTCTGGAAGCATATCTACTATAATTAAGGGAGTTCAGTGCCCCGT 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               $40 TGCAAGCAAAGTTATTACAGTTGGAGCCGTTGACAAGTATGATGTTATAACAAGCTTCTC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     500 AAGCAGAGGCCAACTGCAGAGGCAGGCTTAAGCCTGAGGTTGTTGCTCCAGGAAACTC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660 GATANTIGCTGCCAGAGCAGTGGAACTAGCATGGGTCAATTAATGACTATTACAC 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 CCTCGGCTACGACGGAAGCGGYGTGGTTGCTTGCTCGATAGGGGTATAGACGCGAA 518
                                                                                                                                                                                                                                                                                                                                                                               60 CTTGGGATATGATGCTTCTGGAATCACAATAGGAATAATTGACACTGGAATTGACGCTTC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                     519 CCACCCCGATCTGAAGGCCAAGGTCATAGGCTGGTACGACGCCGTCAACGCCAGGTCGAC 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                           28.34.
                                                                                          ; OTHER INFORMATION: Synthetic
US-09-445-472-2
                                                                                                                                                                                                                                                         Matches 796; Conservative
                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941
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                                                                                                                                                                                                                                                                                                                 305 CAGGAGGGACCTTTACAATGACGGTTAACTCTGGGGCTACAAAGATTACTGGAGACCT 1364
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1296 CAAGGCCATCAAGTACGACGACTAGGCCAAGCTCACCTTCACCGGCTCCGTCGCCGACAA 1355
                                                                                                                                                                      1356 GGGAAGCGCCACCCACACCTTCGAGGTCAGGGGGCGCCACCTTCGTGACCGCCACCCTCTA 1415
                                                                                                                                                                                                                                                                                                                                                                                      1416 CTGGGACACGGGCTCGAGCGACATCGACCTCTACCTCTACGACCCCAACGGGAACGAGGT 1/75
                                                                                                                                                                                                                                                                                                                                                                                                                         1140 TCCAACATCCACAATTAAGCTTCTAAGCTACAGCGGAAGTGCAAACTATCAAGTAGATGT 1199
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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1416 CTGGGACACGGGCTCGAGCGACATCGACCTCTACGACCCCAACGGGAACGAGGT 1475

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18-08-750-532-11

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959 GOTGCAGTIGACAGCAACAACAACGAGCTTCTCCAGCAGGGACCGGGGAC 1017
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                                                                                                                                                                                                                                          598 CACGGAACCCACGTTGCGGGTACCGTTGCCGGAACCGGCAGCGTTAACTCCCAGTACATA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     558 GCCGICGCCCCCGGCGCGCALACTCGICGCGTCAAGGIICICGGTGCCGACGGIICGGGA 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GGGGGGCCCGGGGGGAAGTCGTCGGGGTGTCAGGTTCTCGGTGCCGACGGTTCGGGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   718 ACCOTCTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGGACAAGTACGGG 777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 ATAAGGGCATCAACTCTCCGGCTCCTCCGGAGCTCCGAGGAGCTCCCTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838 AGTCAGGCCGTCAACAACGCCT~GGACGCCGGTATAGTAGTAGTGCGTCGCCGCCGGCAAC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 AGTCAGGCGGTCAACACGCGTGGACGCGGTATAGTAGTCTCGCGTCGCCGCGCGCACC 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 AGGGGCGGAACACCTACACCGTCGCTCACCCGCCGCGCGAGCAAGGTCATAACCGTC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CACGGANCTCACGTGGCGGGAACAGTTGCCGGAACAGGCAGCGTTAACTCCCAGTACATA 63
26.9%, Score 532.8; DB 1; Length 56 97.0%; Pred. No. 3.9e-98; tive. '0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATCON' NATIONAL MATERIAL MATE
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STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
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COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 14, Application US/058948188 ; Patent No. 6261822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DCS/NS-DOS
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WEDLIN TYPE: FLORPY division COMPUTER: IBM PC computible OPERATING SYSTEM: PC-9CS/NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1138 GCCACCCGCACGTTTCG3G 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544 GCCACTCCCCATGTTACCGG_563
Ouery Match
Best Local Similarity 97.0%,
Natches 543; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: TAKAKU
APPLICANT: MORISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
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                                       1020 CTGGGACAATAGCGACCTTGATCTTTACCTCTACGATCCCAATGGAAACCAGGT 1079
                                                                                                                                                            1476 TGACTACTCCTACACCGCCTACTACGGCTTCGAGAAGGTCGGCTACTACAACCCGACCUC 1835
                                                                                                                                                                                                                                                       1536 CGGAACCTGGACGGTCAAGGTCGTCAGCTACAAGGCGCGGCGAACTACCAGGTCGACGT 1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1140 TGGAACATTAAAGTTTAAAGTTGTAAGCTACAGGGAAGTGCAAACTATCAAGTAGATGT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MARCHA MITTON MARCH MARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENDIUM TYPE: Ploppy disk
COMPUTER: IMP PC compatible
SPERATING SYSTEM: FC COOX/AS-LOS
SOFWARE: Patentin Release #1.0, Version #1.30
APPLIANTON MOMBER: US/08/750,532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: BROWNY AND NEIWARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE DESTRUCTION OF THE STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1596 CGTCAGCGACGGGAGCCTCAGCCAGTCCGG 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1200 GGTANGTGATGGTTCCCTTTCACAGCCTGG 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08750532
Patent No. 5756339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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TOPOLOGY: linear MOLECULE TYPE: CDNA NAME/REY: CDS LOCATION: 1.564

Wed Nov

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Patent to 61451.

Patent to 61451.

Patent to 61451.

TITLE OF INFERTION CATENA EL EXCUPTION CATENATION CATENA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 TGATAGACACGGCTTACTTCGGTAACACAAGGGTCTCCGGCCATAAAGTTCATACAGGAGG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            870 Terredadecerrences canceaccecrececres enrescences ereserves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 ATTACAAGGTECAGGTTGALGACGCCACTTCCGTCTCCCAGATAGGGGCCCGATACGGTT 451
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, i.ind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISH: Streptomyces viridosporus
STRAIN: A-914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyccs antibloticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOPTWARE: Wordperfact 9.1
CURRENT APPLICATION DATA
APPLICATION NURBE: U3/09/000,016
FILLING DATE: January 30, 1998
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-721-8293
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 7.7a,
Best Local Similarity 54.54;
Matches 583; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JENTIFICATION METHOL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP 20006
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                        Washington
D.C.
W: U.S.A.
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1078 GGAACCAGCATGGGCACCCGATAAACGACTACTACAGCAAGGGCTCTGGAAGCAGCATG 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 AGTCAGCCGCCAACAACAACGCCTGGGACGCCGGTATAGTAGTAGTCTGCGTCGCCGCGGGAAC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 GGAAGCCTCAAGCCGGAAGTCGTCGCCCCGGCGTTGACATAGCCCCGCGCGCCCAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 ATAAGGSTCATCAACCTCTCCCTCGGCTCCTCCAAGCTCCGAGGAGCGGACTCCCTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 GGAACCAGCAGGGGCACCGGGATAAAGGACTACAGCAAGGCCTCTGGAACCTCAATG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         598 CACGGAACCCACGTIGCGGGTATCGTIGGGGAAGCGGCAGCGTTAACTCCCAGTACATA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          558 GCGFCGCCCCGGGGGGCAAGTCGTCGGCGTCAAGGTTCTCGGTGCGGACGCTTCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          718 AGCGTCTCCACCATCATCGCGGGTGTTGACTGGGTCGTCCAGAACAAGAGAAGAAGTACGGG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  778 ATAAGGGTCATCAACCTCTCCCTCGGCTCCTCCCAGGCTCCGACGGAACCGACTCCCTC 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CACGGAACTCACGTGGCGGAACAGTTGCCGGAACAGGCGTTAACTCCCAGTACATA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.94; Score 512.8; DB 4; Best Local Similarity 97.04; Pred. No. 3.9e-98; Matches 543; Conservative 0; Mismatches 17;
        20-MAY-1998
                                                                                                CLASSIFICATION 435
CLASSIFICATION 435
PRIOR APPLICATION DAYA:
PILLING LATE: 07-NOV-1996
PRIOR APPLICATION DAYA: 323285/1995
APPLICATION NUMBER: JP 323285/1995
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: UP 231285/1995
FILLIG DATE: 12-DEC-1995
FILLIG DATE: 12-DEC-1995
MAME: Broudy, ROGE L.
REGISTATION NUMBER: 25-618
REFERENCE/DOCKET NUMBER: 25-618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 528-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SED ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 GCACTCCCATGTTACCG 563
CURRENT APPLICATION DATA:
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LENGTH: 564 base pairs
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TYPE: nucleic act US-08-894-818B-14 TOPOLOGY:

RESULT 13 US-09-000-016-1

Indels 48; Caps Length 2809;

Score 191.6; DB 3; Pred. No. 7.1e-30; 0; Mismatches 439;

ADDRESSE: wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., #800

CITY: Washington STATE: D.C. COUNTRY: U.S.A.

ED: 2000 PORTION OF THE PROPERTY OF THE PROPER

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ACTICICCTCCACCGCCCCCCCCCCCCCGCGCCCCATCAACCGGACGTCACCGCTC 15/15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1626 AGGGACCGGCCGCCTACATGACCATCTCCGGCACGTCSATGGCGACCCGCACGTCGCG 1685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGTTGGCGCGCTCATCCTCCAGGCCCACCGGACCTGGACCGGCGGCCAAGGTGAAGACCG 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOGGGGGGCGCCTCCTGAAGAGAGAGAGCGCGGACTGAACCTCGGCCGAACTGAAGGGCG 1745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCTCACCGGCTCCACCAAGGGCGCCC----AAGTACACCCCGGTTCGAGCAGGGTT 1796
                                                                                                                              1104 GGCCGGCGGCGGCGACAAGGTGGGCCACCCACCCACGTCGCCTCGATCGCGGGGCA 1163
                                                                                                                                                                                                                                                                                                                                             224 GCAAGGTCCTCGACGACGACTCCGGCACGACTCCGGCATCCTCGGCGATGGAGT 1283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1332 TGGACACACCGGAGACCGACCGCTGGAGGCGGCGGTCGACAAGCTGTCCGCCGAGAAGG 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGTCCTGTTCGCCATCGCGGCGGCAACGAGGGCCG-----GAGTCGATCGGTTGGC 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                989 GCTTCTCCAGCAGGGACCGAC---CGCGGACGGAAGGCTCAAGCCGGAAGTCGTCGCCC 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- AAACGACTACTACACCAAGGCCTCTGGAACCAGCATGGCCACCCCCGCACGTTTCGG 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1217 CCCTCATCGAGACCGCCGACATAGTCGCCCCCAAGGAGATAGCGGACATCGCCTACGGTG 1276
                            047 ACACGAGCCATCAGGACCTGAAGGCCGGGTGA---CCGCGTCCAAGAACTTCACGGCG 1103
                                                                                                                                                                                                         632 CCGGCAGC---GTTAACTCCCAGTACATAGGCGTCGCCCCCGCCGCGCAAGCTCGTCGGCG 688.
                                                                                                                                                                                                                                                             164 coggococongrecandogeanstacandescercocaccescescescercocance 1223
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                                                                                                 572 GGTCGACCCCTACGATGACCAGGGACACGGAACCCACGTTGCGGGTATCGTTGCCGGAA 631
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512 ACGCGAACCACCCCGATCTGAAGGGCAAGGTCATAGGCTGGTACGACGCCGTCAACGGCA 571
                                                                                                                                                                                                                                                                                                                TCAAGGTTCTCGGTGCCGACGGTTCGGGAAGCGTCTCCACCATCATCGCGGGGTGTTGACT 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809 CCCAGAGCTCCGACGGAACCGACTCCCTCAGTCAGGCCGTCAACAACGCCTGGGACGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1857 TCACCTTCGCCGTCCAGCAGTGCCGCACACCGACGAGCCGGTCACC 1906
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Patent No. 6361987
GENERAL INFORMATION:
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TOPOLOGY: lines:
NOLECULE TYPE genomic ONA
ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORGANISM: Streptedyces antibioticus

STRAIN: <Unknown>

NAME/KEY. LOCATION: PEATURE: PEATURE

LENGTH: 2809 base pairs TYPE: nucleic acid STRANDEDNESS: double

REGISTRATION NUMBER: 40,949
REFERENCE/DOOKTY NUMBER: «UNKNOWN»
TELECONMUNICATION: 1NPORMATION:
TELECONMUNICATION: 202-721-8200

TELEFAX: 202-721-8250 SEQUENCE CHARACTERISTICS: TELEX: <Unknown>

APPLICATION NUMBER: 09/000.016 FILING DATE: January 30, 1998 ATTORNEY/AGENT INFORMATION: NAME: Lee Cheng

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1047 ACACGAGCCATCCGGACCTCALAGGCCGOGTGA---CGGCGTCCAAGACTCACGCGCG 1103
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                                                                                                                                                                                                       indels 48
Query Match 9.74; Score 191.6; DB 4;
Best Cocal Similarity 54.54; Pred. No. 7.1e-30;
Matches 583; Conservative 0; Mismatches 439;
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TITLE OF LEWENTION GERE ENCODING A PROTEIN HAVING ASTWORTENCE: THE AUTHOROPHICAL ACTIVITIES ACTIVITIES ASSETTINGED 1.4: CITYLEGERE ACTIVITIES ASSETTINGED 1.4: CITYLEGERE ACTIVITIES ASSETTINGED TO ACTIVITIES ASSETTINGED ASSETTINGED TO ACTIVITIES ASSETTINGED ASSETT
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Length 2809:

LOCATION: 2540..2209
LIDENTIFICATION HETHOD: P
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-514-340.1

LOCATION: 338...2539 IDENTIFICATION METHOD:

NUMBER OF SECURNCES: 7 CORRESPONDENCE ADDRESS:

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990 GC---TCCCCCGCCTACSACGCCTAAGGCCTGACGCCTCTCCCTCCACACGGTGTCC 1046
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1.164 CGGCCCAGTCCAAGGCAACTACAGGCGTCGCCCCCGCGCGCAAGTCGTCGCAGC 688

1.164 CGGCCCCAGTCCAAGGCAAGTACAAGGCGCTGCACCCCGCGCGCCCATCCTCAAG 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1332 TGSACACACGGGAGACCWCCCCTGGAGGCCGCCGGTCGACAGCTGTCCCCCGAGAAGC 1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 GGAACTCCCTCGGCTACGACGGAAGCGGTGTGGTTGCCATCGTCGATACGGGTATAG 511
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Pred. No. 1.4e-29;
0; Mismatches 440; Indels 48; Gaps
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STRAIN: A-914
       UURKENT APPLICATION DATE: US7:9/000,016
FILING DATE: USR:30,000,016
FILING DATE: USR:30,000,016
FILING DATE: USR:30,000,016
FILING DATE: USR:30,000,016
                                                                                                                                                                                                                                                                                                                                         33,367
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TELEPHONE: 202-721-8200
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LENGTH: 2539 Base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE:
ORGANISM: Streptomyces *1
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Matches 582; Conservative.
                                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LCCATION: 338...2535
LDENTIFICATION HETHC.):
US-09-000-016-3
                                                                                                                                                                                                                                                                                                  NAME: Warren M. Cheek.
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                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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1164 COGGCGCCAGTCCAAGGGCAAGTACAAGGGCGTGGCACCCGGGGGCCGCGATCCTCAACG 1223
                                                                      689 TCAAGGTTCTCGGTGCCGACGGTTCGGGAAGCGTCTCGACCATCATCATCATGTGTTGACT 748
                                                                                                                                                                                                                   749 GGGTCGTCCAGAACAAGACAAGTACGGGATAAGGGTCATCAACCTCTCCCTCGGCTCCT 808
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2033 K Street, N.W., #800
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IBM Compatible
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Patent No. 6143541
GENERAL INPORMATION
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MEDIUM TYPE: Disket
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OPERATING SYSTEM:
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COUNTRY: U.
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SUMMARIES

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                GACACCGTCATAATGTTCGGGAGCTACGGAGCAGGGACAGGGCGGTTAAGGTACTGAGG 240
                                                CTCATGGGCGCCCAGGTCAAGTACTCCTACAAGATAATCCCTGGTGTGGGGGGTTAAAATA 300
                                                         241 CTCHTGGGGGGGGGGGGGTANGTACTCCTGCTGTGGGGTTANATA 300
                                                                                 901 AAGGCCAGGGACCTTCTGCTGATCGCGGGCATGATAGACACGGGGTTACTTCGGTAACAAA 360
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GACATOGOCTACGGTGCGGGTAGGGTGAACGTCTACAAGGCCATCAAGTACGACGACTAC 1320
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US/100:0624 Sequence 15, Application Uspatent No. US20020132335A1 GENERAL INFORMATION: RESULT 2 US-10-090-624-15

TYPE: DNA

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                                                                                                                                           107 AGANGANCTATGOTOTGCTAACGCCAGGACTGTTCAGAAAATTCAAAAATTGAATCCTA, 166
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                                                              Score 750.2; DB 12; Length
Pred. No. 1.5e-163;
O: Mismatches 518; Indels
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 64.74:
Matches 1219; Conservative (
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                                                                                                                        1172 TCCTCCAGGCCCACCCGAGCTGGACCCGGGACAAGGTGAAGACCGCCCTCATCGAGACCG
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Settern No. US2002012335A;
GENERAL INFORMATION:
APPLICANT: TAKANURA, MILLAU
APPLICANT: WORSHITA, MIC
APPLICANT: SHINOJO, TORNYC
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APPLICATION NUMBER: PCT/USO1/00667
FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00666
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CTCCAGTGTACTAACGCTCTAAGTCAGGTTATAACGAGGGTGGATGCTGGATTAGT 475
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MPRICATE ARABA RIVER AND AUGUSTA ARABA RIVERTIEROGYALE TITLE OF MENNETING STEPPED FOR EMPRESSION BY CONTRIBUTION OF A CO
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Pred. No. 5.5e-120;
0; Mismatches 371; Indels
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Best Local Similarity 68.0%,
Natches 796; Conservative
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5.74, Score 111.8; DB 10: Length 1635,
Bast Local Similarity 44.84; Pred. No. 6.1e.17;
Matches 514; Conservative 0; Mismatches 627; Indels 6;
PRIOR NELLOGONE, 2001.01-10.
PRIOR MELLOGONE, 2001.
PRIOR MELLOGONE, 2001.01-10.
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OTHER INFORMATION: EXPRESSED IN LUNG.
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Sequence 3471, Application 25/09864761 Sequence 3471, Application 25/09864761 GENERAL IMPORATION: APPLICATE Penn. Sharron G: APPLICANT: Penn. Sharron G: APPLICANT: Rank. Dayld R.

RESULT 5 JS-09-864-761-3471 THE REPORTATION OF COMPANIES AND ADMINISTRATION OF COMPANIES A

PRIOR MEDICATION NUMBER: PC./USOL/00667 PRIOR PELLING DERE: 2001-01-30 PRIOR APPLIANC DATE: 2001-01-30 PRIOR PELLING DATE: 2001-01-30 PRIOR APPLIANCE DATE: 2001-01-30 PRIOR FILING DATE: 2001-01-30

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1386 COGGOCACCTTCGTGACCGGCACCTCTACTGGGACACGGGGTCGAGCGACATCGACCT 1445
               1506 COAGAAGGTCGGCTACTACAACCGGACGGGAACCTGGACGGTCAAGGTCGTCAGCTA 1565
                                                      1446 CTACCTCTACGACCCCANNGGGAACGAGGTTGACTACTCCTACACGGCGTACTACGGCTT 1505
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ORGANISM: Homo sapiens
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Query Match Malarity 4.74; Score 111.8; DB 10; Length 1973; Jesset Local Similarity 4.81; Pref. No. 6:er 17; Indels 6; Gap# Matches 5.14; Conservative 0; Mimatches 62;

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026 CARGCCGGAAGTCGTCGCCCCGGCGTTGACATCATAGCCCCGGCGCGCGAACCAT 1085
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1806 CENCTACCTCFACGACCCCAANGCCACCTTGACAGGTCCAOGTCGAGGAACAACTA 1865 1866 CGAGCACGTCGAGTACGCCAAACACCCGGGAACGTTCCTCGTCTACCTA 1925 1636 CODCOCOLANDOCOLANDOCOLANDOCOLANDOCOLANDOCOCOLANDOCOLA 1686 CTCACCGGTTACCACTAACCACTAACACAACAACAACATCACCATCACCATCAACGTCAA 1745 1746 CAGGGGTGCCAACAAACGGTGACGTGGATACTTCCTACAACGACCTCGA 1805 1386 COGCOCCACCTTCGTGACCGCCACCTCTGGGACACGGGGCTCGAGGGACATCGACCT 1445 1142 CACCATCACCATCACCACCACCACCACCACCACCACCATC----ACTACCA 1197 1446 CTACCFCTACGACCCCAACGGAACGAGGTTGACTACTCCTACCACCGCCTACTACGGCTT 1505 1266 COCCTACOGIGCOGGTAGGGTGÄACGTCTACAAGGCCATCAAGTACGACGACTACGCCAA 1325 1326 GCICACCTICACCGGCCTCCGTCGCCGACAAGGGCCCACCCACCCTTCGACGTCAG 1385 1926 CAGCACC 1932 11 1111 1676 CACCACC 1682 à a

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                                                                                Sequence 4. Application UE/CG7.3033
Patent No. US2020069431A1
GENERAL INFORMATION:
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PRIOR FILLING DATE: 1999-17-
NUMBER OF SEQ ID NOS: 8
US-09-748-033-4
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RESULT 6

Patentin Ver. 2

Length 2712;

OB 10; 5.3v; Score 104.2; TYPE: DNA ORGANISM: Streptomyces alžažoflavus .09-748-033-4 SOFTWARE: Paten SEO ID NO 4 LENGIH: 2712 Query Match

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us-09-841-553-2.rnpb

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FILING DATE: 2001-01-30
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FILING DATE: 2000-09 31
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Patent No. US20020048763A1
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FILING DATE: 2000-06 73
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PRIOR FILING DATE: 2001-01-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
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SOFTHARE: Annomax Sequence:
SEQ ID NO 19241
LENGTH: 1075
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                                                                                                              673 GCGAAGCICGICGGCGTCAAGGTTCTCGGTGCCGAAGGTTCGGGAAGGGTCTCCACCATC 132
                                                                                                                                                                                                857 GCGGGGTCGTCGCTCGCGGTCCCTTCGCCGGGATGGTCGGCCTCGCCCCACC '916
                                                                                                                                                                                                                                                                                   733 ATCGCGGGTGTTGACTGGGTCGTCGTCGAAAGAAGAAGTACGGGATAAGGGTCATCAAC 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    850 AACAACGOCTGGGACGCCGGTATAGTAGTCTGCGTGGCCGGCCGGCAACAGCGGCCGGAAC 909
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2; Mismatches 698; Indels
Best Local Similarity 45.2%, Pre
Matches 591; Conservative 0;
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ORGANISM: Hono sapiens

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SEO ID NOS: 49117
Annomax Sequence Aveting Engine vers: 1.1
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CURRENT FILING DATE: 2001-2%,23
PRIOR APPLICATION NUMBER: US 50/180,312
PRIOR FILING DATE: 2000-02-64
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FILLING DATE: 2001-01-30
APPLICATION NUMBER: FCT/USO1/00651
PILLING DATE: 2001-07: 0
APPLICATION NUMBER: CT/USO1/00670
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PRIOR APPLICATION NUMBER: PCT/US01/00668
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FILING DATE: 2001-01-33
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PRIOR FILING DATE: 2001-01-29
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US-09-864-761-2513/c
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                                                                                                                          OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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ITLE OF INVENTION: HOMAN GROME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL PO ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY Sequence 2513, Application US/09864761 Palent No. US20020048763A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G. APPLICANT: Rack, David R. APPLICANT: Banzel, David K. APPLICANT: Chen, Wensheng

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Query Metch 4.5%, Score 97.8; DB 10; Length 1403; BBE Local Similarity 46.0%, Pred. No. 9.7-14; Indels 14; Gaps Metchae 452; Conservative 0; Missatches 517; Indels 14; Gaps

945 GGTCATAACCGTCGGTGCAGTTGACAGCAACGACAACATCGCCAGCTTCTCCAGCGGG_1004 1005 ACCGACCGCGGACGGAAGGCTCAAGCCGGAAGTCGTCGCCCCCGGCGTTGACATCA7AGC_1064 885 CGCCGCCGGCAACAGCGGGCGGAACACCTACACCGTCGGCTCACCCGCCGCGGCGAACA 944

1065 CCCGCGCGCCAGCGAACCAGCATGGGCACCCCGATAAACGACTACTACACCAAGGCCTC: 1124 ò

1125 TGGAACCAGCATGGCCACCCGGCACGTTTCGGGGGTTTGGCGGGCTCATGCTCCAGGCCCA 1184

1185 CCCGAGCTGGACCCCGGACAAGGTGAAGACCGCCCTCATCGAGACCGCGGACATAGTCGC 1244 1245 CCCCAAGGAGATAGCGGACATCGCCTACGGTGCGGGTAGGGTGAACGTCTACAAGGCCR: 13C4 ò

1365 CACCCACACCTTCGACGTCAGCGGCGCCACCTTCGTGACGGCCACCCTCTACTGGGACAC 3.424

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1425 GGGCTCGAGCGACATCGACCTCTACGACCCCAACGGGAACGAGGTTGACTACTC 1484

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1485 CTACACCGCCTACTACGGCTTCGAGAAGG7CGGCTACTACAACCCGACCGCCGGAACCTG 1544 1605 CGGGAGCCTCAGCGAGTCCGGCGGCGGCAACCCGAATCCAAACCCCAACCCGAACCCAAC .545 GACGGTCAAGGTCGTCAGCTACAAGGGCGCGGGGGAACTACCAGGTCGACGTCGTCAGCGA

1665 CCCGACCACCCACACCCAGACCTTCACCGGTTCCGTTAACGACTACTGGGACACCAGCGA 1724

1725 CACCTTCACCATGAACGTCAACAGGGGTGCCACCAAGATAACCGGTGACCTGACCTTCGA 1784

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1843 ACCTCCACGTCGAGCAACAGCTA 1865

423 CACACTGCACTGATCCACCACTA 401

7-66-054-50-SC

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OTHEN INFORMATION: Desc.or., for of Articles Sequence: Sequence of OTHEN INFORMATION: having a 120 repeat of ACG flanked by fixed of OTHEN INFORMATION: fragments having Nool restriction sites: US-09-790-399-7 ORGANISM: Artificial Sequence PEATURE:

TYPE: DNA

1247 CCAAGGAGATACCGCACATX:2CCTACGGTGCGCGTAGGGTGAACCTCTACAACGCCATCA 1306 Langth 390 Duery Merch 15, 15, Score 64.8; DB 10; Langth 39; Deche Local Similarity \$2.24; Prod. No. 6.8e.11.

**Acches 188; Conservative 0; **Asmarches 172; Indeis ** Query Match

1307 AGTACGACGACTACGCCAAAC NUACCTTCACCGGCTCCGTCGCCCAAGGGAAGCGCCA 1366 1367 CCCACACCTTCGACGTCAGGGGGCCCACCTTCGTGACCGCCACCCTCTACTGGGACACGG 1426 ò g

427 GCTCGAGCGACATCGACCTCTACCTCTACGACCCCAACGGGAACGAGGTTGACTACTCCT 1486 g

1487 ACACCGCCTACTACGGCTTCSAGAAGGTCGGCTACTACAACCCGACCGCCGGAACCTGGA 1546

1547 CGGTCAAGGTCGTCACCTACAAGGGGGGGGGGGGAACTACCAGGTCGACGTCGTCAGCGACG 1606

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WELLOWN: No. 7.
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SOPTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                            Sequence 784, Application US/09887576
Patent No. US20020144047Al
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ORGANISH: Oryza sativa
US-09-887-576-784
RESULT 10
US-09-887-576-784
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LENGTH: 1185
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APPLICANT:
APPLICANT:
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Ouery Match
8.29; Score 83.4; D3 10; Length 1185; 73;
88sH Local Similarity 45;31; Pred No. 19-10;
Matches 383; Conservative 0; Mainsches 36; Indels 6; Geps 2;

APPLICANT

1129 ACCAGCATGGCCACCCGCACGTTTCGGGCGTTGGCGCGCTCATCCTCCAGGCCCACCCG 1188 178 ACCACCAAGGCCACCGTCGACTACGAGAAGATCGTCCGCGACACCTGCCGCGCGATCGGC-237 1189 AGCTGGACCCCGGGACAAGGTGAAGACCGCCCTCATCGAGACCGCCGACATAGTCGCCCCC 1248 238 TTCGTGTGCGACGACGTCGGCCTCGACGCCGACGCTGCAAGGTGCTCGTCAACATCGAC. 297 ò

1249 AAGGAGATAGCGGACATCGCCTACGGTGCGGGTAGGGTGAACGTCTACAAGGCCATCAAG~~3308 298 CAGCAGCOCCAACATCGCGCAGGGGGTGCACGGCCCAACGCGCCCCGAGGAGTSS** 1309 TACGACGACTACGCCAAGCTCACCTTCACCGGCTCCGTCGCCGACAAGGGAAGCGCCACL.1353 1369 CACACCTTCGACGTCACGCCCCACCTTCGTGACGCCCACCCTCTACTGGG---ACACG 1425 358 ATCGGCGCCGCCGACGACCACATGTTCGCCTACCCCACGACGACGCCCCCGAGCTG 4.77 ò

1546 ACGGTCAAGGTCGTCAGCTACAAGGGCGCGGCGAACTACCAGGTCGACGTGGTCAGCGAC 16Q5 1606 GGGAGCCTCAGCCAGTCCGGCGGCGGCAACCCGAATCCAAACCCCAACCCGAACCCAACC 1665 598 GACGAGACCGTCACCAACGAGGAGATGCCGCCGACCTCAAGGAGCACGTCAAGCCG 657 538 AACGACGCCGGCGCCATGGTCCCCGTCCGCTCCACACCGTCCTCATCTCCAACGAGCAC 597 8 ò

658 GTCATCCCCGACAAGTACCTCGACAAAAACCATCTTCCACCTCAACCCTCGGGCUGC 717 %

Application US/09922217 Codes Mitches, Decorate, Newtines, Decorate, Newtines, Daring, New York, Colf. Univ. York Con. Hang, York Co. Thang, York Co. Shall, Carole Lynn Hang, Corole E. Nang, Corole E. Nang, Mang, Corole E. Nang, C Sequence 1058, Application Patent No. US20020076414A1 GENERAL INFORMATION: RESULT 11 US-09-922-217-1058

COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS OF COLDM CANCER AND METHODS FOR THEIR USE MOTICATOR C. TORGET, CONNOCION D. TORGET, C. : ORGANISM: Homo sapiens US-09-922-217-1058 TYPE: DNA

1289 ACCTCTACAAGGCCATCAAGFACGACGACTACGCCAAGCTCACCTTCACCGGCTCCGTCG 1348 Query Match Berlinity 4 (20); Score 69.2; DB 10: Length 15720; Dest Local Similarity 46.2t; Pred No. 4e-10; Matches 277; Conservative " 0; Mantches 323; Indels 0; ò 1349 CCGACAAGGAACCGCCACCACCATTCGACGTCAGCGGCCACCATCGTGACGCCA 1408 ò 8

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1409 CCCTCTACTGGGACACGGGCTCGAGCGACATCGACCTCTACCTCTACGACCCCAACGGGA 1468 5800 ACCACCACCACTACGGTGP 7/C ACCCCAACACCCACCGGCACACAGACCCCAACCAGG 5859

us-09-841-553-2.rnpb

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1649 CCAACCGAACCCAACCGCSACCCAGACCCAGACCTTCACGGGTTCGGTTAACGACT 1708
                                                                                                                                                                                                                                                         1709 ACTGGGACACCAGGGACACCTICACCATGAACGTCAACAGGGGTGCCACCAAGATAACGG 1768
                                                                                                                                                                                                                                                                                                                                                                                                            6100 Accernicheceneceschingagadeceninenesheracenteneenenenesses 6159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1769 GTGACCTGACCTTCGATACTTCCTACAACGACCTCGACCTCTACGTCTACGACCCCAACG 1828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 GGAAGCGGTGTGGTTGGCAYCGTCGAPACGGGTATAGACGCGAAGCACCACTCTG 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        532 AAGGGCAAGGCCATAGGCTGRIACGACGCCGTCAACGGCAGGTCGACCCCCTACGATGAC 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     613 CAGTACCGCGGACCTGCTCTAAGCAGAACTTGTCGGTGTAAAAGTATATGGACAAAATG 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             709 GGTTCGGGAAGCGTCTCCACCFTCATCGCGGTGTTGACTGGGTCGTCCAGAACAACAAGAC 768
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BONEY MRICH
ALCONI SIMILATEY 49:174 PPERG NO. 9 5-54-10.
MRICHOS 406; CORSETVELLY 0; MISMENDED 359; INDELS 60;
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Patent No. US20020146721A1
GENERAL INFORMATION:
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> ORGANISM: Bacillus licheniformis

US-09-974-300-1934
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US-09-974-300-1934
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5980 ACAGAGGCGAACGACGACGACGACCACGACGGGAGGCCCAACGA 6039
                                                                                                                                                                                                                                                                                                                                                                1709 ACTGGGACACCAGCGACACCTTCACCATGAACGTCAACAGTGCCACCAAGATAACCG_1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1769 GIGACCTGACCTTCGATACTTCCTACAACGACCTCGACCTCTACCTCTACGACCCCAACG 1828
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Bast Local Statistry (6.24) Pred. No. 4e-10;
Metches 277; Condervative 0; Mismatches 323; Indels 0;
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7 ORGANISM: Homo septens
US-09-833-263-1058
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US-09-833-263-1058
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APPLICATION TO COOKING AND THE APPLICATION OF THE A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     837 CAGTCAGGCGGTCAACAACGGCTGGGAACGCCGGTATAGTAGTAGTCTGCGTCGCCGGCCAA 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             897 CAGC-GGGCGANCACCTACTC GTCGGCTCACCCGCCGCGCGCGAG-.CAAGGTCATAAC 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1374 CTTCGACGTCAGCGGCGCCACCTTCGTGACCGCCACCTCTACTGGGACACGGGCTCGAG 1433
014 GGACGGAAGGCTCAAGCCGGAAGTCGTCGCCCCGGGGTTGACATCATAGCCCCGGGGC 1073
                                                                                                                                                                                                                                                                                                                    1134 CATGGCCACCCCACCTTTCCTTGCCGCGCTCATCCTCCAGGCCCACCCGAGCTG 1193
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                                                                                                                                                                                                                                                                                                                                                               433 CATCOSCATCGGCATCGGCGTCAGCGTCAGCGTCGGCATCGGCGTCCGCATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 CGTCGGCATCCGCGTCAGCATCATCATCACCTCCGGTCGGCATCGGCATCGG 254
                                                   133 CATCGGGGTCCGCATCCGCGTCCGCATCCGCATCGGCGTCCGCATCCGCATCCG 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1434 CGACATCGACCTCTACCTCTACGACCCCAACGGGAACG 1471
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Patent No. US20020069431A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver.
SEQ ID NO 6
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US-09-748-033-6
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                                  BIL CAGAGCTCCGAACGGAACCGACTCCCTCAGTCAGGCCGTCAACAACGCCTGGGACGCCGTT 870
                                                                                     971 ATAGTAGTOTGCGTCGCCGGCAACAGGGGGCGGAACACCGTACAGCGTCGGCTCACCC 930.
                                                                                                                                                                                                                                               913 GOTGTCACCACAACATTATTACACTCGGAGCCTTGGATGACAGGATACAGTCAGCGG 972
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LOCATION: (1) ... (863)
OTHER INFORMATION: n - A,7,C or G
US-05-974-300-5249
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VERSION KEYWORDS SOURCE ORGANISM

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Missouri, Columbia, MO 62211, USA
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Best Local Similarity (9.3%; Pred: No. 1.7e.05;
Matches 259; Conservative 0; Mismatches 255; Indeis 10; Gapo
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edditive: drug; washing agent: foodstuff; chemicsl synthesis; ds.
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                                                                AAX05926 Standard; DNA: 1977 BP.
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Ouery Match 100.0%; Score 1977; DB 20; Length 1977; BBat Local Similarity 100.0%; Pred No. 0. Mismarches 1977; Conservative 0: Mismarches 1977. Sequence 1977 8P: 453 A; 659 C; 554 G; 311 I; 0 other;

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301 ANGGCCAGGGACCTTC3GCTGATCGCGGGCATGATAGACACGGGTTACTTCGGTAACACA 360 301 ANGGCEAGGGACTTCCCGCGCATCATAGACACGGGTTACTYCGCTACACACA 360 4 20 541 PTORATOGEOGRACAGOS PARAGOGA ACCOCTACOCOS PACA AGACACACA 600
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CTCGACCTCTACCTCTACGACCCCAACGGCAACCTCGTTGACAGGTCCACGTCGAGGAAC 1865
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                                                                       1381 GFCAGCGGCCCACCTTCGTGACCGCCCCCTCTACTGGGACACGGGCTCGAGCGACCCTTATO
                                                                                                                                                                     GOCTTCGAGAAGGTGGGCTACTACAACCGGACCGCGGAACCTGGACGGCCAAGGTCGTC, 1560
                                                                                                                                                                                     GGCTTGGAGAAGGTCGGCTACTACAACCGGACGCGGGAACCTGGACGGTCAAGGTCGTC 1560
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                                                                                                                                                                                                                                             ACCTACAAGAGGCGGGGGGAACTACCAGGTCGACGTCGTCAGCGACGGAGCCTCAGCTAG
                                                                                                                                                                                                                                                                             TCCGGCGGCGGCACCCGAATCCAAACCCCAACCGGAACCCAACCCGGACCACGACACÇ^1680
                                                                                                                                                                                                                                                                                               CAGACCTICACCGGITCCGITAACGACIACTGGGACACCAGCGACACCTICACCAIGAAC 1740
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1321 GCCAAGCTCACCTTCACCGGCTCCGTCGCCGACAAGGGAAGCGCCACCACACCTTCGAC 1380
               1921 OCCIRCROCACCIACOGCIGGGCGGACIACCAGGICAAGGCCGICGICIACIACGGG 1977
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                                                        1381 GTCAGCGGCCACCTTCGTGACCGCCACCTCTACTGGGACACGGGCTCGACGACAC
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S. Yamamoto K;
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754 AGGACAAGTACGGGATAAGGGTCATCAACGTCTCCCTCGGCTCCTCGCAGAGCTCCGACG 823
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                                                                                                                                                                                                                                                                                                                                  68.6%; Score 1360.8; DB 18; Length 1977; 83.9%; Pred. No. 7.3e-242; tive 0; Mismatches 292; Indels 9; C
                              Protesse(s) and genes encoding them obtained from Thermoococus bycococcus strains - have artices the thing thermal stability and useful industrially and as respect the sequences.
                                                                                                                                                                                                                                                                               Sequence 1977 8P; 527 A; 562 2; 513 G; 375 T; 0 other;
                                                                                                                               Claim 11; Page 95-97; 159pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 83.9
Matches 1573; Conservative
                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                           Thermococcus protesse frequent coding sequence
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                                                                                                         AAT85677 standard; DNA; 3859 BP
                                                                                                                                                                                                                                                                                                          Thermococcus celer DSH-2476.
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                                   1004 GACOGRACGGGAAGGGAAGGCTCANGCCGAAGTCGTCGCCGCGGGGGTGACATCATACT 1063
11004 GACCGAACGCGAACGGGAAGGTCAAGCGGAACTCGTCGCCGCGGGGGTTGACATCATAC_1063
                                                                                                                                                                                            1064 CCCCCCCCCCACCGGAACCAGCATGGGCACCCCGATAAACGACTACTACCCAAGGCCT 1123
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884 TCGCCGCCGGCCAACAGCGGGCCGAACACCTACACCGTCGGGCTCACCCGGCCGCGGGGAGCA 943
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Pyprococcal furfices and this produ. as a recombinet portes. 
In transformate using a vector carrying the protease game 
(AMPSHAI). A genomic to the sequence of the transformation is given in 
AVPSHAI and its encoded grotein in AMRS/09 streams.
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in the specification"
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a bear of position 587 is not identified in the specification.
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in the specification,"
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recombinant prodn. of hyper-thermostable protesse
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                                                                                                                                  526 GATCTGAAGGGCAAGGTCATAGGCTGGTACGACGCCGTCAACGGCAGGTCGACCCCTAC 585
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                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                          646 TCCCAGTACATAGGGGTCGCCCCGGGGGGGAACCTCGTCGGGGTCAAGGTTCTCGGTGCC 103
                                                                                                                                                                                                                                                                                                                                  106 GACGGTTCGGGAAGCGTCTCCACCATCATCGGGGGTGTTGACTGGGTCGTCCAGACAACAAG 765
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Sequence 898 BP; 192 A; 299 C; 266 G; 130 7; 11 other;
                                                    Query Match
888t Local Similarity 97:04; Pred. No. 1.1.
Matches 874: Conservative 0: Mismatches
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7)14 Sequence represent t figness. If the additions going to the sequence for the additions of the addition of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Processes 19 and genes encoding then obtained from Thermococcus and 
the hard stealing and as research fight thermal stability and are 
useful industrially and as research research research.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morishita M, Takakura
                                                                                                                                                                                        Thermococcus protease fragment coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                      Phermococcus celer DSM-2478'.
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Isunasawa S, Yamamoto K;
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1697 ATGACAGGAGGACACCTTTACATGACGTTACCTCTGGGGGCTACAAAGATACTGGGGGT 17:6
1697 ATGACAGGAGGACACCTTTACATGACGTTACCTTGGGGGCTACAAAGATAATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGTTACATGACGACGACATGACATGACGACGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATGACATATACATG
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Recombinant hyperthermostable protease from Pyrococcus furiosus - 
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ttive 0; Mighatches 618; Indeis 48; Gaps
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                                                                                                Asada K, Kato I, Morishita M, Shimojo T,
                                                                                                                                                                   DiscLosure; Page 59-60; #2pp; Japanese.
                                                                                 (TAKI ) TAKARA SHUZO CO LTD.
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Matches 1219; Conservative
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        Pyrococcus furiosus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1392 CATACAAGGCTATAAACTACGAAAACTATGCAAAGCTAGTGTTCACTGGATATGTTGCCA 1351
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                                                                                                                                                                                                                                                             812 AGAGCTCAGATGGTAGCGCTCTAAGTCAGGCTGTTAATGCAGCGTGGGATGCTGGT 87.
                                                                                    572 GPFATCCAFACGAFGACGAFGGACATGGAACTCAFGAGGFTCAATAGCAGCTGGFACTG 531
                                                                                                                                   632 GAGCAGCANGTAATGGCAATATAAAAGGTCCAGGAGCTAAGCTGGCGGGAATTA 691
                                                                                                                                                                                                                             692 AGGTTCTCGGGTGCCGAACGGTTCGGGAAGGGTCTCCACCATCGTCGGGGTGTTGACTGGG 751
                                                                                                                                                                                                                                                                                                                                                                                                                      812 AGACCTCCGACGGACCGACTCCCTCAGTCAGCGGCGAACAACAACGCCGGGACGCGGGT 8/1
575 CGNCCCCCTACGANGACCAGGAACCCCACGTTGCGGGTATCGTTGCGGAACCG 634
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This sequence represents coding sequence for the protease from 
Pyrococcus in the foreign by the coding sequence for the protease of the 
invention. The protease give an invention have extremely high thornal 
smothling in protease give an end as research research, and 
reduction the protease give and chemical industries.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1652 ACCGGAACCCAACCCCGACCAACACCCAGACCTTCACGGTTCCGTTAACGACTACT 1711
                                                              1712 GGCACCAGGGACACCTTCACCA73ANCGTCAACAGCGGTGCACCAAGATAACCGGTG 1771
                                                                                                                                                                                                                                                 1197 ATGACAGGAGGGGACCTTFACAATGACCGTFACTCTGGGGGCTACAAAAATTACTGGAG 1756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1882 ACCTOSTIGACAGGTCCACGTUGAGCAACAGGTACGAGCACGAGCCCG 1891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1817 AGCTTGFAGATAGATCGGAGAGFCCCAACAGGTACGAACACGGFAGAATACTTAACCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protesse(s) and genes enrouting them obtained from Thermococcus or syrococcus strains - have extremely high themsal stability and useful industrially and pig research respense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_ercept= (pos: 1282..1284, as: Xaa)
/note= "%%"= Gly, Val*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus furiosus protects coding sequence.
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1.1566
/*tag= e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Teunasava S. Yemamoto K.
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P-PSDB; AAW24122.
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Sequence 1566 BP; 467 A: 342 C: 372 G, 384 T; 1 other;

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4PI; 1959-080907/07. P-PSDB, AAM94836. W09856926-A1. 04-JUN-1998; 10-JUN-1997; 17-DEC-1998. AAX05920, AX05920 35.0%; Score 692.8; Da 18; Length 1566; 57.1%; Pred. No. 8.6e.119; 24.0 0; Mismatches 483; Indels 18; Gaps* 459 CCPCGGCTACGACGGAAGGGGTGGTGGTTGCGATCGTCGATACGGGTATAGAGGCGAA 528 60 CTTGGGATATGATGGTTCTGGAATCACAATAGAAAAATTGACACTGGAATTGACGCTTC 119 519 CONCCCGNICTGANGGCCAAGGTCATAGGCTGGTACGACGCGGTCAACGGCAGGTCGAC 578 960 TGATAACAAGATAAGTACGAAATTAAGTCATAATCTTCTTCTTGGTCAAGCCAGAG.419 579 CCCCTACGATGACCAGGGACACGGAACCCAGGTTGCGGGTATCGTTGCCGGAACCGGGGG 1638 180 TCCATACCATACGATCGACATCGACATCATCATCTACATACCACTGGTACTGGACC 239 639 CG---TIMACTCCCAGIACAIAGGCGTCGCCCCCGGGGGGAAGCTCGICGGCGTCAAGGT 695 240 AGCAAGTAGGCAAGTACAAGGGAATGGCTCCAGGAGCTAAGCTGGCGGGAATTAAGGT 299 696 TCTCGGTGCCGACGGTTCGGGAAGCGTCTCCACCATCATCGGGGGTGTTGACTGGGTGGT 755 100 TCTAGGTGCCGATGCTTCTGGAAGCATATCTACTATAAGGAGTTAAGGCGGTT 359 756 CCAGAACAAGGACAAGTACGGGATAAGGGTCATCAACCTCTCCCTGGGCTCCTCCCAGAG 815 CTCCGACGGAACCGACTCCCTCAGTCAGGCCGTCAACAACGCCTGGGACGCCGGTATAGD 875 420 CTCAGATGGTACTGACGCTCTAAGTCAGCTGTAATGCAGCGTGGGATGCTGGATTAGT-479 336 COCCARCANGGTCATAACCGTCGGGGTTGACAGCAACGACAACATCGCCAGCTTCTC 995 996 CAGCAGGGACCGACGGACGGAAGGCTCAAQCCGGAAGTCGTCGCCCCCGGGGFTTA_1055 1056 CATCATAGCCCCGCGCGCGCGGGGAACCAGCATGGGCACCCCGATAAACGACTACTACAT 1115 1116 CANGGCCTCTGGANCCAGCATGGCCACGCCGCACGTTTGGGGCGTTGGCGGCCTCATCGC/11175 1176 CCAGGCCCACCGAAGCTGAACCCGGAAAAGTGAAAGACGGCCTCATCGAGACGGCGA 1235 1236 CATAGT GGCCCCAAGGAGATAGCGGACATCGCCTAGGGTGCGGGTAGGGTGAACGTCTA" 1295 1296 CANGGCOATCAAGTACGACGACGAAGCTCACCTTCACCGGCTCGGTCGCGACAA 1355 1356 GGGAAGCGCCACCCACCTTCAACGTCAGCGGCGCCACCTTCGTGACGGCCACCCTCTA 1415 CTGGAAACGGGCTCGAGCGACCTCGACCTCTACGACCGCAACGGGAACGAGGT 1478 600 ANGCAGAGGGCAACTGCAGAGGCAGGCTTAAGCCTGAGGTTGTTCTCTCCAGGAACTG 659 840 TATCSTAAAGCCAGATGAAATAGCCGATATAGCCTACGGTGCAGGTAGGGTTAATGCATA 899 900 CAAGGCTATAAACTAGGATAACTAAGGAAGGTAGGGTTGACTGGATATGFTGGCAACAA 959 Matches 1020; Conservative Local Similarity

Hyperthermostable proteass fragment encoding DNA. AAX05920 standard: DNA; 1236 BP 06-MAY-1999 (first entry)

Myperthermostable; proteas:: thermophilis; becterium; subtilisin; additive: drug; washing agont; foodstuff; chemical synthesis; ds. Asada K, Kato I, Morishiga N, Shimojo T, Takakura H; 98WO-JP0245: (TAKI) TAKARA SHUZO CO LITT. 97JP-01519* Pyrococcus furiosus.

Recombinant hyperthermostable processe from Pyrococcus furlosus and gene encoding it, for Ease scale production of the protesse for hodustrial use.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            900 TCTAGGTGCCGGATGGTTCTGGAAGCATATCTACTATAATTAAGGGAGTTGAGTGGGCCGT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 CCAGAACAAGGACAAGTACGGGATAAGGGTCATCAACCTCTCCCTCGGCTCCTCCCACAG-815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 CITGGGATATGATGGTTCTGGAATCACAATAGGAATAATTGACACTGGAATTGACGCTTC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       519 CCACCCGAICIGAAGGGCAAGGTCAIAGGCIGGTACGACGCCGGTCAACGGCAGGTCGAC 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 579 CCCCTACGATGACCAGGGACACGGAAACCCACGTTGCGGGTATCGTTGCCGGAACCGGCAG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 TCCATACGATGACATGAAACICATGTAGCTTCAATAGCAGCTGGTACTGGAGC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 MCCARGTATGCCARGTACAGGGATGGCTCCAGGAGCTARGCTGGCGGGAATTAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.3%; Score 560.4; DB 20; Length 1236; 58.0%; Pred. No. 2.1e-94; Live 0; Mismatches 371; Indels 3; Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1236 BP; 368 A; 251 C; 309 G; 308 T; 0 other;
Claim 6; Page 37-38; 82pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 58.0
Matches 795; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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1475
                                                                   1296 CAAGGCCATCAAGIACGAGG; CÂAGGCCAAGCTCACCGGCTCCGTCGCCGACAA 1355
                                                                                                                                                                           960 AGGCAGCCAAACTCACCAGTICG/TATTAGGGAGCTTCGTTCGTAACTGCCACATTATA 1019
                                                                                                                                                                                                                                                                                                           1536 CGGNACCTGGACGGTCAAAGGTCGTCAGCTACAAGGGCGCGGCGAACTACCAGGTCGACGT 1595
                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus furiosus hyperwisestmostable protease gene - useful for recombinant prodn. of hyp. thermostable protease
                                                                                                                                           GGGAAGCGCCACCCACACCTTTTACGTCACCGCCACCTTCGTGACCGCCACCTTA
                                                                                                                                                                                                                   CTGGGACACGGGCTCGACCGACATCGACCTCTACCACCGCCCAACGGGAACGAGGT
                                                                                                                                                                                                                                   1020 CTGGGACAATGCCAATAGCGACAGTAGCTCTAGCTCTAGCAATGGAAAGCAGGT
                                                                                                                                                                                                                                                                                       1476 IGACIACTOCIACACCSCCTAUTACGGCITCGAGAAGGTCGGCTACTACAACCGGACCGC
                                                                                           Length 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a jene (AAT08141) that codes for a hyperthermostable protest; (AAR87007) of Pyrococcus furlosus AAT08133-21) are provided encoding peptides (AAR87010-11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trungsava
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 564 BP; 121 A; 135 C; 161 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease: hyperthormostable; thermostability; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.98; Score 532.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morishita M,
                                                                                                                                                                                                                                                                                                                                                                                                                                   1596 CGTCAGCGACGGAGCCTCAGCCAGTCCGG 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1200 GGTANGTGATGGTTCCCTTTCACAGCCTGG 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4: Page 65-57; 85,47; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Asoda K, Kato I, Mitta E,
Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.79-0130236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT08134 standard; DNA; 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 1996-049674/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR87011.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT08134;
                                                                                                                                                                                                                               9111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1078 GGAACCAGCATGGGCACCACCATACACTACTACACCAAGGCCTCTGGAACCAGCATG 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 CACGGAACCCACGTTGCGGGTATCGTTGCGGGAACGGGCAGCGTTAACTCCCAGTACATA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    718 AGCGTCTCCACCATCATCGCGCGCGTGTTGACTGGGTCCAGAACAAGGACAAGTACGGG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 AGCTCTCCACATATACGCGGGTGTTGACTGGGTGCTCCAGAGATAGGGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    778 ATAAGGGTCATCAACCTCTCCCTCGGCTCCTCCCAGAGCTCCGAAGGGAAGGGAGTCCTC 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 ATANOSQUANCACTOTCCCTCGGTCCTCCCAGAGCTCGAGGGGAGCCGACTCCCTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Processe(s) and sense enboding them obtained from Thermococcus and Pyrococcus strains - New extreactly ligh thermal stability and are useful industrially and iss research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          898 AGCGGGCGAACACCTACAGGGTCGGCTCACCGGCGGCGGGGGGAGGTCATAACGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       484 GGANCCAGCATGGSCACCUCGATAAACGACTACACACGAAGCCTCTGGAACCTCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                  asymmetric hydrolass; dhpA 4-substituted-1,4-dihydropyridine;
derivative; Streptomyces viridosporus; ester; chiral; synthesis;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 564 BP: 121 A: 185 C; 161 G; 87 7; 0 other;
                                                                                                                                                        Disclosure: Page 110-112; 159pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces viridosporus dapa gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT61454 standard; DNA; 3539 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1138 OCCACCCGCACGTTTCGGG :157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S44 GCCACTCGCCATGTTACCGG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-1997 (first entry)
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AAT61454
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                                       O. Caps
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                                                                         598 CACGGAACCCACGTTGCGGGTATCGTTGCCGGAACCGGGCAGCGTTAACTCCCAGTACATA. 657
                                                                                                                                                                         658 GGCGTCGCCCCCGGCGCAAQCTCGTCGGGTCAAGGTTCTCGGTGCCGACGGTTCGGGA, 717
                                                                                                                                                                                                           64 GGCGTCGCCCCCGGGGCGCGAAGGTCGTGGTGTCAAGGTTCTGGGTGCGGCGGTTCTGGGA_123
                                                                                                                                                                                                                                                                               718 AGGTCTCCACCAICATCGCGGGTGTTGACTGGGTGGTGCAGAACAAGGACAAGTACGGG 777
                                                                                                                                                                                                                                                                                                                 124 AGGRETCEACACATCATCCCGGGGTGTTGACTCGGTGCTGCGAAAAAGGATAAGTACGGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                       838 AGTCAGGCGGTCAACAACGCCTGGGACGCGGTATAGTAGTAGTCTGGGTCGCCGGCCAAU 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1978 GGANCGAGGATGGGGACGCGGATNANGAGTAGTAGACCGANGGCGTCTGGAACCAGCATG 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protesse: research respent; thermal stability; thermococcus celer; ss.
                                                                                                                                                                                                                                                                                                                                                                                     Indels
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     97.0%; Pred. No. 2,5e-89;
tive 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermococcus protease fragment coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1138 GCCACCCGGCACGTTTCGGG 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA785576 standard; DNA: 564 8P
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Tsunasawa S, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-JP03253.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermococcus celer DSM-2476
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Best Local Similarity 97.01
Matches 543; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-1998 (first entry)
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37-NOV-1996: 12-DEC-1995; V09721823-A1 9-JUN-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the Streamynew viridosprus Glay down which encore an asymmetric hypothasa witch ents no 4-samestitude 11, distributed table of contracting the contracting of 4-samestitude 11, distributed to 6-samestitude 11, distributed 
                                                                                                                                                                                                                                                                                     145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1047 ACACGAGCATCCGGACCTGAAGGCCCGGGTGA---CCGCGTCCAAGAACTTCACCGCGC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1104 CGCCGGCGGGGGGGAAGGGGGCCACGCACCACCACCCCCATCGCGCCGGCAT153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1164 CGGGGGCCCAACGAACGAACAAGGCGTCGGACCCGGGGGCGCGCGAACGTCAACG 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 GGTCGACCCCTACGATGACCAGGACACGGAACCCACGTTGCGGGTATCGTTGCCC4AA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512 ACGCGAACCACCCCGATCTGAAGGCCAAGGTCATAGGCTGGTACGACGCCGTCAACGGCA 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 TGATAGACACGGGGTTACTCGGGTAACACGAGGGTCTCGGGGCATAAAGTTCATACAGGAGG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                870 TGTGGGACGCGGTCACCAACGGCGACGGCCCCTCCGGCATCGCCCCACGCTCGCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 ATTACAAGGTICAGGTIGACGACGCCACTTCCGTCTCCCAGATAGGGGCCGATACCGTCT 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              930 Acegogrecochececececercanchegrecoresecharesecececenages 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGANCTCCCTCGGCTACGACGGAAGCGGTGTGGTGGTTGCCATCGTCGATACGGGTATAG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   689 TCANGGTTCTCGGGTGCCGACGGTTCGGGAAGCGTCTCCACCATCATCGCGGGTGTTGACT 748
cardiovascular, treatment; hypertension; ischaemic heart disease, ds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9 71; Score 191.6; DB 18; Length 2539; State Local Similarity 9.19; Pred. No. 2e-26; Matches 939; Conservative 0; Nimmatches 439; Indels 48; Cape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asymmetric hydrolase gene derivad from Streptomyces viridosporus -
ate on 4 substituted 1.4 dl. hydro:pyridine derivatives to produce
chiral derivatives useful for synthesis of cardoomscular druys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isshiki K, Matsufuji M, Nakashima
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                                                                                                                                                     Claim 3; Page 49-55; 78pp; Japanese.
                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96W0-JP02147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95JP-0212975
                                                            Streptomyces viridosporus
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P-PSDB; AAM13666-67.
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1121 GCAAGGTCCTCGACGCACTCCGCCACCCCGCATCCTCGCCGGCATGGAGT 1283
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                                                                                                                                                                                                                                                                                                                                                                           1392 GCGCCCTGTTCGCCATCGCGCGCCAACGAGGCCCCG-----GAGTCGATCGCTTCGC 1445
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derivative; Steptomyess, yitidoprus; ester; chiral; synthesis;
oxidioxacular; treatment; hypertension; isohaeut heart disease;
                                                                                                                                          1284 gee------cooccoceccoceccoscoscoscoscoscoscoscos
                                                                                            749 GGGTCCTCCAGAACAAGGACAAGTACGGGATAAGGGTCAJCAAGCTCTCCCTCGGCTCCT
                                                                                                                                                                                                             809 CCCAGAGCTCCGACGGAACDSACTCCCTCAGTCAGGCCGTCAACAACGCCTGGGACGCCG
                                                                                                                                                                                                                                                                                                                                    869 GIATAGIAGTETGUGUGUEĞÜĞĞĞĞĞARARAGGĞĞĞĞĞĞANÇARÇATARACÇGTÇĞĞÇTÇAÇ
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/product
/note= rtcm 5. viridosporus*
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Chimeric Streptomyces a cibi-octous
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mat protein

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1332 TOGACACACCGGACCGACCGGCGGGGGGGGGGGGGGGGACCTGTCCGCCGAGAAGG 1391
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                                                                                                                                                                                                                                                                                                                                         939 CCGCCCCCCGAGCAAGGTCATAACCGTCGGTCCAGTTGACAGCAACGACAACATCGCCA 988
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    Yonsell subtilisin-like secine protesse coding sequence

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Best Local Similarity 54.5%; Pred: No. 26-26;
Matches 583; Conservative 0; Mismatches 439; Indels 48; Gups
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isshiki K. Matsufuji M. Makashima T;
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/*tag* c
/product- Melanin
/note* *from S. antibioticus*
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95JP-0212975.
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Tsuruta T, Yoshioka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SAOC ) MERCIAN CORP.
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P-PSDB; AAW13658.
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31-JUL-1995;
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New DNA sequence of thermophilic protein decomposition enzyme and protein derived therefrom .
P-PSDB; ABB09483
 SXCCXXXXXXXX
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Claim 1, Page 6; 15pp; Korean.

This sequence represents the DNA encoding the Thermosaserobacter yonself subtilisin-like serine protesse of the invention. Sequence 2121 BP; 712 A; 410 C; 425 G; 554 T; 20 other;

ä 374 TAAAGTICAIACAGGAGGATTACAAGGTICAGGTTGACGACGCCACTTCCGTCTCCCAGA 433 Query Match 1211; Score 180.6; DB 21; Length 2121; SB 88st Local Shailarity 55.79; Perdo No. 212-24; Anteches 355; Conservative 0; Mismatches 299; Indels 15; Gapes

443 TIGGAATCACAAAAGCACGAGTGATTTTGGAGTCACAGGAAAAAATATAACAA 502 434 TAGGGGCCGATACCGTCTGGAACTCCCTCGGGTACGAAGGGGTGTGGTGGTTGCCA 499:

GGTACGACGCCGTCAACGGCAGGTCGACCCCCTACGATGACCAGGGACACGCAACCCACG²610 563 GGNAAGACTTTATCAACAACAAAACTACACGACGACAACAATGGCAACTCCACG 622 227

TTGCGGGTATCGTTGCCGGAACCGGCAGCGTTAACTCCCCAGTACATAGGCGTCGCCCCCG 670 623 TAGCANGTATTGCTGCAGGTACAGGTGCTGCAAACAGTCTTTACAAAGGCGTTGCTCTG T6 882

803 ATTIAAGCITCGGCACTICTACAAGTICTGATGGAACTGACTCTACCTCATTAGGACTGK E63 851 ACAACGCCIGGGACGCCGGTATAGTAGTCTCTGCCGCCGGCCGGAACAGCGGGCCGAACA (1)

923 ANTACACCATAGGGTCCCCTGGTGCTGCGGAAAAAGCCATAACAGTCGCAGCAATGGCAG 932

983 ATCHARGTGAACTIGGCTTZAACCTTGCAAGCTTTTCCAGCGGGGTGCTACTGCTGAGG 1042 DIS GAAGGETCAAGCCGGAAGTCGTCGCCCCGGCGTTGACATCATAGCCC 1067 1043 GAAGAATAAAACCTGACATTGCGGCCCCAGGATATAATATAATATAACTGCGGC 1091

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Copyright (c) 1993 - 2002	nduno en	ow protein - protein search, using sv model	October 31, 2002, 13:25:03 / Search time 10 Seconds (without alignments) 2439.921 Hillion cell ands	US-09-841-553-5 3128 1 MKGLKALILVILVIGLVVGS	BLOSUM62 Gapop 10.0 , Gapext 0.5	747574 seqs, 111073796 residues	Total number of hits satisfying chosen parameters:	Minimum DB aeg Length: 0 Maximum DB aeg Length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing (irst 45 summaries	A.Genesec 032802:+	/SIDS1/gcgdata/geneseq/genesegp-emb1/AA1980.DAT:*	/SIDS1/gcgdt.tz/geneaes/geneaeq-enb1/AA1982.bAT:+ /SIDS1/gcgdt.tz/geneaes/geneaeq-enb1/AA1982.bAT:+ /SIDS1/gcgdt.tz/geneaes/geneaeq-enb1/AA1982.bAT:+ /SIDS1/Gcgdt.tz/geneaes-y/geneaeq-enb1/AA1982.bAT:+	/SIDS1/gcgdata/geneseqp /SIDS1/gcgdata/geneseqp	/SIDS1/9cgdata/ganeseq/geneseqp /SIDS1/9cgdata/geneseq/geneseqp		Sibsi Sibsi		/SIDSI/godderz/geneseq/geneseqp-enbl/AA1995.DAT:*	/SIDSI/gcgddta/geneseq/geneseqp-enbl/AA1997.DAT	/SIDSI/gradata/geneseq/geneseqp-embl/aA1999.DAT: * /SIDSI/gradata/geneseq/geneseqp-embl/AA2000.DAT: * /SIDSI/gradata/aneseq/geneseqp-embl/AA2000.DAT: *	The series of th	score greater than or equal to the score of the result being printed	eriore cocal acore		Match Length DB ID		654 20	85.0 659 20 AAW94840 68.5 522 18 AAW34122	\$22 20 412 20	237 168 18 18 17	
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This sequence is a proteined of the remedien Two proteases of the
invention have actuarily high thermal resolutive. The proteases of the
used as recently respectively and industriality in the food, drug and
observed industries.
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                                                                                                                                                                                                                                                                                                                                                                                                           Protease(s) and genes encoding them obtained from Thermococcus-
sprococcus strains. A have brincanely infinitement stability and
useful industrially and as research respents.
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                                                                                                                             95JP-0323285
                                                                           96NO-JP03253.
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Tsunasawa S, Yamamoto K;
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N-PSDB; AAT85695.
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                                           This sequence is a processe of the invention. The processes of the invention have extremely high thermal stability. The processes can be ach as research respects, and industrially in the food, drug and chemical industries.
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ilarity 100.0%; Pred, No. 2.3e-209;
Conservative 0; Mismatches 0;
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      Claim 9; Page 92-95; 159pp; Japanese
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This sequence topresents the protease from Thermococcus celer DSW-2476. This sequence is a protease of the investion, The processes of the invention have extremely high thermal stability. The processes can be used as repeatch resignits, and industrially in the food, drug and hemical industries.
              GPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermococcus protease.
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CDLY LYDPHGHLYDRSTS SNSY EHVEYANPAPGTWTFLVY AYSTYGMADYOLKAVVYYG 659
                   596 LOLYLYDPHOKLVDRSESPHSYCHUTPAPGTWYPLVYAYYYVGNAYYELTAKVYYG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 2997.5; DB 20; Length 654;
; Pred. No. 4.78-182;
22; Mismatches 50; Indels 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKGLKALILVILVLGLVVGSVAAAPEKKVEQVRNVEKNYGLLTPGLFRKIQKLNPNEEIS 60
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                                                                                                                                                                                                                                                                                                                                  Hyperthermostable; protease: thermophilic; bacterium; subtilisin; additive; drug; washing agent; foodstuff; chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant hyperthermostable protease from Pyrococcus furiosus and gene encoding it, for large scale production of the protease.
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                                                                                                                                                       AAW94841 Standard; Protein: 654
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86.34;
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                                                                                                                                                                                                                                                                                           Hyperthermostable protease
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Matches 582; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Pyrococcus furiosus.
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industrial use.
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17-DEC-1998.

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Gaps 7:
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                                                                                                                                                                                                                                                                                                                                                     233 LCADGSGSISTIIKGVEHAVDNKDKIGIKVINLSLGSSQSSDGTDSLSQAVNANDAGIV (292
                                                                                                                                                                                                                                                                                                                                                                  293 VCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASPSSRGPTATGRIKPEVVAPGVD 352
                                                                                                                                                                                                                                                                                                                                                                                                                              3-3 IIAPRASGISMGIPINDYYIKASGISMAIPHYSGVGALILOAHPSWIPDKYKTALIZIAD 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 IIAPRASCTSNGTPINDYTTKASGTSMATPHVSGVGALILGAHPSNTPDKVKTALIZTAD 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 WDTGSSDIDLYLYDPNGNEVDYSYTAYYGFEKVGYYNPTAGTWTVKVVSYKGAARYQVDV 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 VSDGSLSOSGGGNPNPNPNPNPNPTTDTOTRTGSVNDYHDTSDTFTMNVNSGATKITGDL 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     533 VSDGSLSQSGGGNPNPNPNPNPNPTPTTDTQTPTGSVNDYHDTSDTFTMNVNSGATKITGDL.592
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                                                                                                                                                         58 EISTVIVFENHREKEIAVRVLELMGAKVRTVYHIIPAIAADLKVRDLLVISGL--TG--G-133
                                                                                                                                                                                                                                                                                        13 HPDEOGKYIGHVDFVNGRSYPYDDHGHGTHVASIAAGTGAASHGKYKGNAPGAKLAGIKV 232
                                                                                                    1 MKGLKALILVILVIGLVVGSVANAPEKKVEQVRN---VERNYGLLTPGLFRKIQKLNPNE'S7
                                                                                                                                                                                                                            114 KAKLSGVRFIQEDYKVTVSAELEGLDESAAQVMATTVWN-LGYDGSGITIGIIDTGIDAS
                                                                                                                                                                                                                                                       119 NTRVSGIKFIQEDYKVQVDDA----TSVSQIGADTVWNSLGYDGSGVVVALVDIGIDAN
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                                                                      Indels 16:
                                           Length 659;
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                                        Score 2914; DB 18;
Pred. No. 9.46-177;
                                                                      47; Mismatches
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                                        85.08;
Best Local Similarity 83.74;
Matches 558; Conservative 45
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Gaps 22 28

Indels 16: Length 659;

119 NTRYSGIKFIOEDIKVQVDDA-----SYSOIGADTVANSLGYDGSGVVVAIVDTGIDAN 173 IIAPRASGISMCTPINDYYTKASGISMATPHYSGVGALILQAHPSHTPDKVKTALIETAG 412 353 IIAPRASCISMGTPINDYYIKASGISMATPHVSGVGALILQAHPSWTPDKVKTALIETAD 412 IVAPKEIADIAYGAGRVM 2 N. IKYDDYAKLIFIGSVADKGSATHIFDVSGATRVIATLY 472 TVAPKETADIAYGAGRVANYYLAIKYDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLY 472

114 KAKLSGVRFIQEDTKVTVSAELEGLDESAAQVMATYVAN-LGYDGSGITIGLIDTGIDAS

173 HPDLQGKVIGHVDFVNGRSYPYDDHGHCTHVASIAAGFGAASNGKYKGMAPGAKLAGIKV 232

233 233 353 13 13

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58 EISTVIVPENHREKEIAVRVLELMGAKVRYVYHIIPAIAADLKVRDLLVISGL--TG--G 113

1 MKGLKALILVILVIGLVVGSVANAPEKKVEQVRN---VEKNYGLLTPGLFRKIQKLNPNE

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Opery Match

85.04; Score 2914; D8.20;
Best Local Similarity 83.74; Pred. NO. 9.4e-177;
Best Local Similarity 83.74; Pred. NO. 9.4e-177;
Profice 558; Conservative, 47; Hismatches 46;

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the liventure retains to "imperferences destrived from a submanishing between the submanishing the submanishin
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                                                                                                                                                                                                                                                                                                                                           Shinojo T. Takakura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure: Page 55-58; App; Japanese
                                                                                                                                                                                                                                                                                                                                           Asada K, Kato I, Morishita M,
98WO-JP02465
                                                                                                              97JP-0151969
                                                                                                                                                                                                                            (TAKI ) TAKARA SHUZO CO LTD
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04-JUN-1998;
                                                                                                              10-JUN-1997;
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The lovestion relates "ro"s hyperthermostable process derived from as work-mophilic bactarin (separchally processus futuses). The processe has vorking telegratures 40-110 deg.C (optimum 80-55 deg.C), working pf 5-10
61 PYDDHGHGTHVASIAAGTCAASNGKYKGMAPGAKLAGIKVLGADGSGSISTITKGVRWAV 120
                                   253 DHKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAMDAGIVVCVAAGHSGPHTYTVGSPAA 312
                                                         313 ASKVITVGAVDSHDNIASFSSRGPTADGRLKPEVVAPGVDIIAPRASGTSHGTPINDYYT 372
                                                                                                                                 181 ASKVITVGAVDKYDVITSFSGRGPTADGRLKPBVVAPGMMIIAARASGTSMGPPINDYYT 240
                                                                                                                                                                                          373 KASGTSMATPHVSGVGALELQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVY 432
                                                                                                                                                                                                                                  241 AAPGTSMATPHVAGIAALLLQAHPSWTPDKVKTALIETADIVKPDRIADLAYGAGRVNAY 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                               553 NPTPYTDTQTPTGSVNDYWDTSDTFTMNVNSGATKITGDLTPDTSYNDLDLYLYDPNGNL 612
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and gene encoding it, for large scale production of the protease for
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additive; drug; washing agent; foodstuff; chemical synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the protease from Pyrococcus furiosus DSH-1558. This sequence is a protease of the invention, The proteases of the invention have extremely high thermal subality. The proteases can be used as research reasonate, and industrially in the food, drug and
                      S33 VSDCSLSGSGGGGNPENPHPHPTPTDTQTFTGSVHDYMDTSDTFTHÄNVASGATKITGDL 592,
                                                                                593 TEDTSYNDLDLYLYDPRGNLVDRSTSSNSYEHVEYANPARGTWTFLVYAYSTYGWADYQL 652
    533 VSDGSLSQSGGGNPNPNPNPNPNPTPTTDTQTFTGSVNDYNDFSDTFTHNVNSGATKITGDL 592
                                                                                                          133 AELEGLDESAAOVNATYVWHLGYDGSGITIGIIDTGIDASHPDLQGKVIGWVDPVNGRSY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 PYDDHGIIGTHVASIAAGTGAASHGRYKGUAPGAKLAGIKVLQADGSGSISTIKGVSAQX 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Processe(s) and gense encoding them obtained from Thermococcus and)
Pyrooccus strains - have extremely high thermal stability and are:
useful industrally and as research respents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protesse; research reagent; thermal stabillty; pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.5%; Score 2349.5; DB 18; Length 522:
85.2%; Pred. No. 4.5e-141;
1.ve 22; Mismatches 51; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. Takakura H:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 87-90; 159pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualiflers
428
                                                                                                                                                                                                                                                                                                              ANW24122 Standard; Protein; 522 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus furiosus processe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus furiosus DSM-3638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kato I, Mitta M,
S, Yamamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-3P03253
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                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Matches 449; Conservative
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653 XAVYYG 659
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                                                                                                                                                                    653 XAVVYYG 659
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Misc-difference
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AAW24122
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to the commune 6%, and contains more than 400 of its extravely after 6 minus.

11 St day, C. The invention also provides peas sequences encoding 54 people of Commune 5500-100 (19/4) ware 100, and set 501 at a 515 period from smillish, and 700 is 10% above processes, 1000 colls period from smillish, and 700 is 10% above processes, 1000 colls period from the commune of the commune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 PYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVLGADGSGSISTIIKGVENNV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PYDDGGGGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKVIGADGSGSISTIIKGVEMAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 KAIKYDDYAKLTPIGSVADKGSATHTPDVSGATEVTATLYMDTGSSDIDLYLYDPHGNEV 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 KAINYDNYAKLVETGYVANKGSQTAQEVISGASEVIATLYMDNANSDLDLYLYDPNGNQV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 DYSYTAYYGFEKVGYYNPTAGTWTVKVVSYKGAANYQVDVVSDGSLSOSGGGNPNPNPNP-552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553 NPTPTIDICTFTGSVNDYHDISDTFTMNVNSGATKITGDLFFDTSYNDLDLYLYDPNGNL, 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 QPEPTVDAKTFQXSDHYYYDRSDTFTWTVNSGATKITGDLYFDTSYHDLDLYLYDPHQKL 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Gapé
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AELEGLDESAAQVMATYVWNLGYDGSGITIGIIDTGIDASHPDLQGKYIGWDPVNGRSY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KASGTSMATPHYSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVY
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additive; drug; washing agent; foodstuff: chemical synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20; Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           476 VDRSESPNSYEHVBYLTPANGTHYFLVYARTTTGMAXXELTARVYYG 522
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 68.5%; Score 2349.5; DB 20
Best Local Similarity 85.2%; Pred. No. 4.5e-141.
Recticles 469; Conservative 22; Mismatches 51.
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                                                                                                                                                                                                                                                                                                                                                            522 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AELBGLDESAAQVWATYVWNLGYDGSGITIGIIDTGIDASHPDLOGKVIGWDFVNGRSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 KASGTSHATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVY
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                                                                                                                                         Takakura
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Pred. No. 7.8e-114;
                                                                                                                                         Shimoio T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Misnatches
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                                                                                                                                         Morishita N.
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97JP-0151969
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Matches 367; Conservative
                                                                        (TAKI ) TAKARA SHUZO CO
                                                                                                                                                                                                   WPI: 1999-080907/07.
                                                                                                                                  Asada K, Kato I,
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industrial use.
       10-JUN-1997;
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ID AAR8
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Hyperthermostable protease

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26-JUL-1994; 13-JUN-1994;

famamoto K;

Asada K.

W09534645-A1 35-JUN-1995; 21-DEC-1995.

Story William

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This Requese represents it framen of the process term processes futures DNS-1558 less ANXIII2 for full length appearance). This sequence is a framework of the professor of the future and the future of the professor on being a second transmitted to the food, drug and phenical Industrial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 EVISGLTGGKAKLSGVRFIQEDYKVTVSAELEGLDESAAOVMATYVWNLGYDGSGITIGI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 IDTGIDASHPDLQCKVIĞMVDFVNGRSYPYDDHGHCTHVASIAAGTGAASNCKYKGMAPG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IDTGIDASHDDLQGKVIGWVDEVNQRSYPYDDRGHCHHVASIAACTGAASNGKYKGWAPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LVISGLTGGRAKLSGVRRIQEDYKVTVSARLEGLDESAAQVKATYVWNLGYDGSGITIGI 60
                                                                                                                                                                                                                                                                                                        Protesse(s) and ganss snooding them obtained from Thermococcus Strongers Strains - they extracely high termal stability and useful industrially and as research reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.2%; Score 864; DB 18; Length 168;
100.0%; Pred. No. 1.8e-47;
tive: 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takakura H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protease; hyperthermostable; thermostability.
                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 118-119; 159pp; Japanese.
                                                                                                                                                                                                 Morishita M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR87011 standard; Peptide; 188 AA.
                                                                                                                                                                                              Kato I, Mitta M,
S, Yamamoto K;
                                                                                       96NO-JP03253
                                                                                                                          95JP-0323285
                                                                                                                                                              CTAKI ) TAKARA SHUZO CC LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95WO-JP02095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94JP-0173912
94JP-0130236
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                                                                                                                                                                                                                                                 WPI; 1997-332794/30.
N-PSDB; AAV03761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 168; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrococcus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide sequence.
                                                                                                                                                                                                                 Tsunasava S,
               W09721823-A1
                                                                                       07-NDV-1996;
                                                                                                                      12-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A09534645-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1994;
                                               19-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR87011;
                                                                                                                                                                                                 Asada K.
ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 DLOGKVIGWVDPVNGRSYPYDDHGHHVASIAAGTGAASNGKYKGHAPGAKLAGIKVLG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 ADGSGSISTIIKGVEMAVDNKDKYGIKVINLSLGSSOGSOGTDSLSOAVNNAWDAGIVYČ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ADGSGSVSTIACVDHYVQNKDKYGIRVINLSLGSSQSSDSDSLSQAVNNAMDAGIVVC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1051.5; DB 17; Length 237; Pred. No. 3.6e-59; 9; Mismatches 18; Indels 1, Cane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DEKGKYIGHYDAVIGKSTPYODGGHGTHYAGIVAGIYSAV-HSQYIGVAPGAKLYGYKULG-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease; reaearch reagent; thermal stability; pyrococus furiosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrococcus furlosus hyper:thermostable protease game · useful for recombinant prodn. of hyper:thermostable protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the hyperthermostable procease of 
processor furtions and its produ. as a recombinant probe. 
In transforments using a vector carrying the process game 
(ANOBLI). A general CNA sequence of the invention is given 
ARTOBLI) and its encoded protein in AMRNO09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 APRASCTSMGTPINDYYTKASCTSMATPHVSGVGALILQAHPSWTPDKVKT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 APRASGTSMGFPINDYNKGSGSSHOTPHVSGVGGLILQAHPSHTPDKVKT 230
                                                                                                                                                                                                                                                                                                                                                            Mortahita M, Tsunasawa S;
                                                                                                                  /note- 'unspecified amino acid'
           Protease: hyperthermostable; thermostability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3: Pags 70-71; 85pp; Japanese.
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMP24127 standard, Protein; 168 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pyrococcus protease fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 87.9%;
Matches 203; Conservative
                                                                                                                                                                                                                                                                 94JP-0173912
94JP-0130236
                                                                                                                                                                                                                                                                                                                        TAKI ) TAKARA SHUZO CO LID.
                                                                                                                                                                                                                                                                                                                                                            Kato I. Mitta M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus furiosus DSM-3638
                                                                                                                                                                                                                             95WD-JP01095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 1996-049674/05.
                                               Pyrococcus furlosus
                                                                                               Misc-difference 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 237 AA;
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RESULT 10 AAW24127

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Nakashina T:

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110 LTGGKAKLSGVRFIQEDYKVTVSAELEGEDESAAQVMATYVWNLGYDGSGITIGIIDTGI 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 DASHPOLOGKVIGWVDFVNGRSYPYDDHGHGPHVASIAAGFGAASNGKYKGMAPCAKLAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 DTSHPDLKGRVTASKNFTAAPG-AGDKVGHGTHVASIAAGTGAQSKGKYKGVAPGAAILN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 GKYLDDSGPGDDSGILAGNEWAA----AQCADYVNMSLGGMDTPE-TDPLEAAVDKLSAE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AGIVVCVAAGNSGPHTTTVGSPAAASKVITVGAVDSNDNIASFSSRGP-TADGRLKPEVV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 APGVDIIAPRASGTSMGTPIND---YYTKASGTSMATPHYSGYGALILOAHPSWTPDKYK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 GAL--TGSTKGGK-YTPREQGSGRIQADKALQOTVIADPVSVSFGVQQMPHTDDEPVTKQ 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Naymmetric hydrolase gele derived from Streptomyces viridosporus ente on «subsituted-1%—di hydropytdinh defivatives to produce chiral derivatives to produce chiral derivativas to bedge sprichesis of cardiovascular drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IXVIGADESSESTITIKGYBYAVDNKOKYGIKY INLSLGSSOSSOGTOSLSOAVNY-AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular: treatment: hypertension; ischaemic heart discase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match

26.21; Score 692.5; DB 18: Langth 823;
Best Local Smilarity 33.64; Pred No. 11.8-35;
Natches 202; Conservative 62: Mismatchee 223; Indess 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim S. Page 37-43; 78pp. Japanese.
                                                         Chimeric Streptomyces viridosporus.
Chimeric Streptomyces antibioticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arisawa A. Dobashi K,
Tsuruta T, Yoshioka T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAOC ) HERCIAN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-145682/13.
N-PSDB; AAT61455.
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                                                                                                                                                                                                                                                                                                                                                                                    M09705243-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-301-1996:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-FEB-1996:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                             51:
                                Telegopous appropriate proventie for a proventie for a propriate production of the Stagnard control of
                                                                                                                                                                                                                                                                                                                                                    ; Score 692.5; DB 18; Length 734;
; Pred. No. 9.1e-36;
62; Mismatches 223; Indets 115; Géps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  asymmetric hydrolase; dhph. 4-substituted-1,4-dihydropyridine; idetivative; Streptomyces viridosporus; ester; chical; synthesis; [55]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 LTGGKAKLSGVRFIQEDYKVTVSAELEGLDESAAQVMATYVWNLGYDGSGITIGIIDTGI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 VINGDRIASGIAHVALD ---- GVRRAALDTSVGQIGAPKAWSAGYDGKGVKIAVLDTGV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 DASHPDLOGKVIGWVDFVNGRSYPYODHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 IXVLGADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSGAVNN-AMD 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 APGVDITAASAEGNDIGQEVGEGPAGYHTISGTSMATPHVAGAAALLKQOHPDWTSAELX 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 GAL--TGSTKGGK-YTPFEGGSGRIQADKALQOTVIADPVSVSFGVQQWPHTDDEPVTKQ S25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----YDDYAKLTFTGSVADKGSATHTFDVSGATFVTATLYWDTGSSDIOLYCYDPN 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 LTYRNLGTQDVTLKLTSTATDPKGKAAPAGFFTLGATTVTVPA---GGSASVDMTADTRL 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   489 CNEVDYSYTARYGFEKVGTYNPTAGTWTVKVVSY-----KGAANYQVDVVSDGS 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTVDGAYSAXVVATGGGGTVRTAAAVOREVESYDVTVRHIGRDGKPTTEHLTDLIEFAG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                643 LGSGRGYG ------APATDTATLRLPXGTYLVDSWIAKDFGTLKGGIDWLVQPKLSV 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 TKITGDL/FOT-SYNDLDLYLYDPNGNLVDRSTSSNSYEHVEYANPAPGTWTFLVYAYST 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 AGIVVCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGP-TADGRLKPEVV. 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 APGVDIIAPRASGTSMGTPIND -- - YYTKASGTSMATPHVSGVGALILQAHPSWTPDKVK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 LSQSGGGNPNPNPNPNPNPTPTTD7QTF---TGS-VNDYMDTSD7FTW-----NVNSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          694 TKDT-TLTLDARTTKAADITVPDPK------AKPLSAT--IGYTVDT
Page 49-55; 78pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ž
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                                                                                                                                                                                                                                                                                                                                                    33.64;
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity ....
Natches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DhpA-mel chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                          734 AA;
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Claim 3;
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Best Local S
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Ë Nakashima

Isshiki K, Natsufull M,

/noce= "see AAMissucce" see AAMissucce 735.822 "mclanin (percial sequence)"

95W0-JP02147 96JP-0067478 95JP-0212975

/label - DhpA_protein_product

Location/Qualifiers

21,

12337 A. . 10s

è è	417
ò	489 GNEVDYSITAXIGFEKVGYINPJAGIHTVKVVSY
g	583 GGTVDGAYSAYVATGGGQTVRTAAAVQREVESYDVTVRHIGRDGKFTTEHLTDLIGNG, 642.
à	538 LOQSGGGNPNPNPNPNPNPNPNPNPNPNPNPNPNPSNNVNSGA.585
q	643 LOSGRGYGAPATDTATLRLPKGTYLVDSHIAKDFGTLKGGIDWLVQPKLSY,693
ò	586 TKITGDLFFDT - SYNDLDLYLXDPMGNLVDRSTSSNSYEHVEYANPAPGTHTFLVYAVST 544.
g	694 PKDT-TLTLDARTTKAADITVPDPKAKPLSATIGYTYDT 731.
ó	57 KB 646
a	732 AG 733
RESU	SESSULT 15
80	AAN13666 standard; protein; 520 AA.
12	AAW13666;
Z L	06-OCT-1997 (first entry)
Y S	Fragment of dhpA gene product.
X 2 2	esymmetric hydrolase; dhpA; 4-substituted-1,4-dihydropyridine: deriyative; Streptomyces viridosporus; ester: chiral; svothesis:
X :	cardlovascular; treatment; hypertension; ischaemic heart disease.
So	Streptomyoes viridosporus.
Y E E	Key Location/Qualiflers
L	
11	Misc-difference 238 /note= "Ser238 as indicated in the specification"
X Z	HO9705243-A1.
ž £	13-PEB-1997.
× å	30-JUL-1996; 96HO-JP02147.
× 2 2	1961-1996, 96JP-0067478.
××	(SAOC) MERCIAN CORP.
XII	Arisawa A. Dobashi K. Isshiki K. Matsufuji M. Nakashima T
×	WPI; 1997-145682/13.
×	N-PSDB, AAT61454-55.
ttt	T Asymmetric hydrolase gene derived from Streptomyose viridosporus. The arcts on "submittuded" 1-401 hydrolysidian derivatives to produce 1. The control derivatives aseful for synthesis of cardiowseniar drugs.
X S	Claim 1; Page 60-63; 78pp; Japanese.
ž88	This sequence is a fragment of an asymmetric hydrolase which arts on
388	the hydrolase (DhpA) was isolated from the chromosomal DNA of
388	Streptomyles withdospinus, The enzyme alions the entitient convecsion of 4-substituted-1,4-dihydropyridine esters to chiral partially hydrolysed destrotives, for use in the synthesis of cardiovascular-drugs

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258 YGIXVINLSLGSSQSSDGTD&LSQAVNN-AHDAGIVYCVAAGNSGPNTYTVGSPAAASKV 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 ITVGAVDSNDNIASFSSRGP-TADGRLKPEVVAPGVDIIAPRASGTSMGTPIND---YYT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 LIVGAVDOKDKLADFSSTGPRLGDGAIKPDVTAPGVDITAASAEGNDIGGEVGEGPAGYM 232
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                                                                                                                                                                                                                           Gapa
                                                                                                                                                                                                                                                                                  138 LDESAAQVMATYVWNLGYDGSGITIGIIDASHPDLOGKVIGNVDFYNGRSYPYDDH 197
                                                                                                                                                                                                                                                                                                                                                1 LDTSVGQIGAPKAWSAGYDGKGVKIAVLDYGVDYSHPDLKGRVTASKNFTAAPG-AGDKV 59
                                                                                                                                                                                                                                                                                                                                                                                                              198 GHGIHVASIAAGTGAASNGKYKCHAPGAKLAGIKVLCADGSGSISTIIKGVEHAVDNKDK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 GHGTHVASIAAGTGAQSKGKYKGVAPGAAILNGKVLDDSGFGDDSGILAGMEHAA----A 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 KASGISMATPHVSGVGALILGAHPSWIPDKVKTALIETADIVAPKEIADIAYGAGRVNVY 432
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suitable for the treatment of e.g. hypertension and ischaemic heart disease.
                                                                                                                                                                                                                           79,
                                                                                                                                                Query Match 19.84, Soore 679.5; DB 18; Length 520; Best Local Stallarity 36.34, Pred. No. 196-39; Matches 181; Conservative, 55; Mismatches 183; Indels 79;
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Job time : 33 secs
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543.5 15.9 353.7 US-07-923-260A-2 543 15.8 362.7 US-08-460-3438-3 543 15.8 3737.7 HS-08-38-258-2 543 15.8 3737.7 HS-08-38-2	540.5 15.8 1398 1 US-08-750-532-9 540.5 15.8 1398 4 US-08-894-8188-8	540.5 15.8 1598.4 US-09-445-472-6 537.5 15.7 360 1 059-07-918-318-2 537.5 15.7 360 2: US-08-413-724-2 537.5 15.7 360 3: US-09-049-867-2	18 577-5 15.7 380 4 US-0553-464.2 Sequence 2. APPLI 19 577-5 15.7 380 4 US-05-76-793-1 Sequence 2. APPLI 40 577-5 15.7 380 4 US-05-76-793-1 Sequence 2. APPLI 41 577-5 15.7 380 6 5272878-2 Sequence 2. APPLI	15.7 380 6 5336511-2 15.6 377 -1 08-07-772-087-2 15.6 382 2 08-08-504-2658-75	15.5 274 4 US-09-104-623A-3	SLEGNINGS	T L'INSUL	US-08-884-818B-5 Sequence 7. Application US/08894818B Factor No. 625821 Lon US/08894818B GREEAL INFORMATION	APPLICAMT: TAKAKURA, HİXATU S APPLICAMT: HORISHITA, MÜ APPLICAMT: TAKAKURA, KATSUNIKO	APPLICANT: WITTY, MASSAINCET APPLICANT: TSUKSAWA, KIYOZO APPLICANT: TSUKSAWA, SUSSAWA WATCH TAYON, TRANSPARIA PROFESSIONAL TAYON, TRANSPARIA	WINTE OF THE SERVICES: 42 COURSES OF THE SERVICES OF THE SERVI	9	COUNTRY: United States of America	COMPUTER TRANSPORTED OF COMPUTER COMPUTER TENT COMPUTER TENT FOR C	SUFTWARE SISTEM FULL DOS/MS-DOS SUFTWARE Patentin Release #1.0, Version #1.30 CURRENT APPLICATION PRAG	: APPLICATION NUMBER: US/08/894,818B ; FILING NUMBER: 10-MA-1998 CLASSITIONATION - 3-3-6	PRIOR APPLICATION NUMBER: PCT/JP96/03253	FILING DATE: 07-NOV-1996 : PRIOR APPLICATION DATA	FILICATION NUMBER: JF 323285/1995 FILICATION NUMBER: JF 323285/1995 FILICATION NUMBER: JF 323285/1995	NOMEZIACEN TROPINALIUM NECESTRATION NUMBER: 55.618	REPERENCE/DOCKET NUMBER: TAKANDRA-1 TELECOMMUNICATION INFORMATION:	TELEPHONE: (202) 628-5197	SECURITION FOR SEQ ID NC 5: SEQUENCE CHARGERSTICS: LEMTH. 659 MIN. 5.	TYPE: anino acid TYPE: anino acid TYPE: anino acid TYPE: anino acid	NOLECULE TYPE: peptide
GenOcre version 5.1.3 Copyright (c) 1993 - 2002 Compagen Ltd.	etn - pro	Run on: October 31, 2002, 13:28:38 search time 13 Seconds (vilhout alignment) 1238.190 Aillion cell updates/sec	TILIE: 105-09-841-551-5 Perfect sorre: 342 Perfect	Scoring table: 8LOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 231628 seqs, 24425594 residues	Total number of hits satisfying chosen parameters: 231628	Minimum Da seq langth: 0 Maximum Da seq langth: 200000000	Post-processing: Winiams Match 0% Asatams Secto 100% Lizar 4 summaries	Detabase: Issued, Patents, AA;* 1. Yesp1.2, Fordete.AJ, Jan.5A, COMB. PSP: 2. Yosp1.2, Fordete.AJ, Jan.5A, PSP: 2. Yosp1.2, Fordete.AJ, PSP: 2. Yosp1.2, Fordete.AJ, Jan.5A, PSP: 2. Yosp1.2, Fordete.AJ,	31 Coptac Syptement Annual Ann	Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is detrived by analysis of the total bring printed.	SUMMRIES	Result Query No. Score Match Length DB ID	US-08-894-8188-5 US-08-894-8188-35	87.4 654 4 US-09-445-472-16 Sequence 16, 85.0 659 4 US-08-894-8188-1 Sequence 1.	522 4 US-08-48-472-4 Sequence 12: 522 4 US-08-894-818B-3 Sequence 3: 522 4 US-09-445-472-4 Sequence 4:	56.0 412 4 US-09-445-472-1 Sequence 1.	692.5 20.2 823 4 US-09-000-016-2 679.5 19.8 520 4 US-08-000-016-2	557 16.2 379 1 US-08-685-774-2 Sequence 2, 555 16.2 382 4 US-09-445-472-31 Sequence 2,	554.5 16.2 378 1 US-07-772-087-4 Sequence 4.5	554 15.2 379 3 US-09-140-933-1 Sequence 1, 554 15.2 379 4 US-09-146-551-1 Sequence 3, 554 15.3 379 4 US-09-146-551-1 Sequence 3,	551 16.1 382 4 US-09-150-12-1 Sequence 17. 551 16.1 382 4 US-09-255-502-2 Sequence 27. 550 16.0 18.5 6 417866.5	549.5 16.0 381 1 US-07-772-087-6 Sequence 549.5 16.0 381 1 US-08-173-508-12 Sequence	16.0 381 2 US-08-265-310-12 Sequence 12., 16.0 381 3 US-08-951-742-12 Sequence 12., 16.0 382 4 US-09-178-155-2 Sequence 2. A	27 545 15.9 350 1 US-07-923-260A-4 Sequence 4, Appli

us-09-841-553-5.rai

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1S-08-894-818B-S
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61 TVIVEBNERKELAVRVLZIJGAKVRKYYHIIPAIAADLKVRDLLVISGLTGGKAKLSGV 120
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                                                                          Patentin Release #1.0, Version #1.30
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Pred. No. 2.5e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: TAKAKURA-1
TELECOMMUNICATION INPORMATION:
                                                                                                          URRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/894,8188
FILING DATE: 20-MAY-1998
                                                                                                                                                                                                              CARACHECATION DATA:
APPLICATION NUMBER: PCT/F96/03253
PILING DATE: 07-NOV-1996
PRIOR APPLICATION DAVA:
APPLICATION NUMBER: 09-323485/1995
FILLING DATE: 12-D6-1895
                                                        PC-DOS/HS-DOS
                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-INS/MS-
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 88.3%
Matches 582: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 654 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Browdy, Roger L.
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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MOLECULE TYPE: peptide
                                                                                                                                                                                                 CLASS IFICATION:
REDIGH TYPE:
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                                                                                 OFTWARE:
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                                                                                                                                                                                                              MKGIKALILVILVIGUTVOGSVAAAPEKKVEQVRNVEKNKGLLTPGLFRKIGKLNPNEEIS 60
                                                                                                                                                                                                                                                                                  TVIVESNHREKEIAVRVLELMGAKVRYYHIIPAIAADLKVRDLLVISGLTGGKAKLSGV 12D
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                                                        100.0%; Score 3428; DB 4/ Length 659;
100.0%; Pred. No. 1.1e-241;
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COUNTRY: United States of America
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Patent No. 6261822
                                                                                                                      datches 659, Conservative
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121 RETGEDYKYTYSAELGGLDSSAAOWARTYWNICZYGGSGIFIGIIDTGIDAGDASHPOLGGKV 180
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601 LOKYLYDROGNLYDRSTSSNSTEHVEYANDROFWTELVKARSTYGANDYOLKAVVYTG 559
LOLKYLYDROGNLYDRSSSNSTEHVEYANDROGNTFLUKARTTYGANTYELTAKVYVY 559
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88.3%; Pred. No. 2.5e-210;
Live 22; Mismatches 50; Indela 5;
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MATLONE, SASA, MYSON
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 16, Application US/09445472
Patent No. 6358726
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US-09-445-472-16
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COMPUTER: IBM PC COMPACIDLE
OPERATING SETEM, PC COSS/SS-COS
CONTANER: PEDERIC NEL OMARIA BL.O., VETSION 11.30
CURRENT PARLICATION NUMBER: US/OB/S94.BISB
FILING DATE: 10-144-1598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.H., Ste. 300
IITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 85.04; Score 2914; Best Local Similarity 83.79; Pred, No. 3e-Notches 558; Conservative, 47; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 323285/1995
FILING DATE: 17 DEC-1957
ATYORNEY/AGRAT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAKAKURA-1
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                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/088948188
Patent No. 6261822
GENERAL INFORMATION: 48
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TELEPHONE: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1...
SEQUENCE CHARACTERISTICS:
LENGTH: 659 mm.ho. acids
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RECISTRATION NUMBER: 25.
REFERENCE/DOCKET NUMBER:
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TOPOLOGY: linear
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HOLECULE TYPE: peptide
US-08-894-8188-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
NEDIUN TYPE: Floppy
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US-08-894-8168-1
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533 VSDGSLSQSGGGNPNPNPNPNPNPTPTIDIQFPTGSVNDTWDTSDTFTMNVNSGATKITGDL 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 KAKESGVRFIQEDYKVTVSARABGLDRSAAQVNATVVNN-LGYDGSGITIGIIDTGIDAS 172
                                         119 NIRVSGIKETQEDYKVQVDDA-----TSVSQIGADTVANSLGYDGSGVVVAIVDTGIDAN 173
                                                                                                                                                                                                                                                                                                                             293 VCVAAGNSGPNTYTVGSPAAASÄVITVGAVDSNDNIASFSSRGPTADGRLKPEVVAPGVD 352
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER, INS PC COMPUTER, DO
OPERATING SESTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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419 Soventh Street N.W., Ste.
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APPLICATION NUMBER: US/08/894.818B
FILING DATE: 20-MAY-1998
CLASSISTICATION: 435
PRIOR APPLICATION DATA:
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GEREBO TRYNOMATION
APPLICANT MARKANDA, BIKATU
APPLICANT MARKANDY, Ke'suhik
APPLICANT STANAMATO, Ke'suhik
APPLICANT STANAMATO, Kasuncui
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1 Sequence 3, Application US/U8894818B
1 Patent No. 6261822
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MEDIUM TYPE: Floppy
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STATE: D
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                                                                                                                                                                                                                                                                       IVAPKEIADIAYGAGRVNVYKAIKYDDYAKLTETGSVADKGSATHTFDVSGATFVTALLY 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 HPDLQGKVIGWVDFVNGRSYPYDDHGHGTHVASIAAGTGAASNGKYKGMAPGAKLAGIKV 232
                                                     174 HPDLKGKVIGWYDAVKGRSTPTDDGGHGTHVAGIGSV-NSQYIGVAPGAKLVGVKV 232
                                                                                                                                   LGADGSGSISTIIKGVEMAVDNKDKYGIKVINLSLGS8QSSDGTDSLSQAVNNAMDAGIV 292
                                                                                                                                                                       293 VCVAAGNSGPNTYTVGSPAAASKVITVGAVDSNDNIASFSSRGFTADGRLKPEVVAPGVD 352
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Patent No. 6358776
GENERAL INFORMATION:
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GRANISM: Thermococcus celer
US-09-445-472-12
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653 KAVVYYG 659 653 KAVVYYG 659 CS-09-445-472-12

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133 ABLEGLDESAAQVMATYVHNIGYDGSGITIGIIDTGIDASHPDLGGKVIGWVDFVNGRSY 192
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Seat Local Similarity 85.2%; Pred. no. 2.7%-128.
Seat Local Similarity 85.2%; Pred. no. 2.7%-128.
                       APPLICATE TREA, LINEAR TREA, PROPERTY REPRESENTANCE THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OFFI
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TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE
FILE REPREME, TAKAKURA-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    613 VDRSTSSNSYEHVEYAHTAPGTWTFLVYAYSTYGWADYQLKAYVYYG 659
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LOCATION: (428)...(428).
DTHER INPORMATION: Xea at position 428 is Gly or Vel.
US-09-445-472-4
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Patent No. 6358726
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pyrogoggus furzügus
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APPLICANT: HORISHITA, Ni-
APPLICANT: SHIMOJO, TOMOKO
APPLICANT: SADA, KLYOZO
APPLICANT: KATO, IKUNOSHIN
                                                                                                                                                                                                                                                                                                                                                       SEC ID NO 4
LENGTH: 522
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US-09-445-472-1
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Selvocal Similarity 85.73; Pred. No. 27-65;
Moschow 449; Conservative 22; Mismarchos 45; Indels 5; Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ASKVITVGAVDKYDVITSFSSRGPTADGRLKPEVVAPGNWIJAARASGTSNGQPINDYYT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             493 DYSYTAYYGPEKYCYYNPTAGTHTVKVVSYKGAANYOVDVVSDGSLSQSGGUPNDNPNP 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 NPTPTTDTQTFTGSVNDYHDTSDTPTHNVNSGATKITGDLJFDTSYNDLDLYLYDPNGNL 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 QPEPTVDANTFQXSDHYYDRSDFFTHTVNSGAFKITGDGVFDTSYHDLDCXLVDPHQKL 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THER INFORMATION: /note= xaa at position 428 is Gly or Val
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MACHICLIO MUSIC ETC/1958/01233

MACHICLE DATE: CT-409/1233

MACHICLIO MUSIC ETC/1959/01233

MACHICLIO MUSIC ETC-1953

MACH
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Patent No. 6358726
GENERAL INFORMATION:
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APPLICANT: HORISHITA, MLO
APPLICANT: SHINOJO, TOMOKO
APPLICANT: ASADA, KLYOZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
PEATURE:
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US-09-445-472-4
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ORGANISM: Pyrococcus furiosus US-09-445-472-1

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LENGTH: 412 TYPE: PRT

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DERREAL INFORMETTERS.

APPLICATION ALTER AND RE CALLE A POTENT MATERA SENSITIVE DE TITLE OF TREATMENT CON LONG ENGOGENE A POTENT MATERA SENSITIVE DE L'ACASTONIC DES ENGOGENE NATURE CAL «BESTITATED 1.4 CANTERDEPRIDE DE TITLE OF TREATMENT PER TITLE DE SENSITIVE DE L'ACASTONIC SENSITIVE DE L'ACASTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 ADGSGSISTIIKGVEWAVDNZDKTGIKVINLSLGSSQSSDGTDSLSQAVNNAWDAGIVVC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ADGSGSVSTILAGUDWNVDNKXXTGIRVINIALGGSGSGGTGSLGANNANDAGIVVC 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1045.5; DB 1; Length 237;
Pred. No. 8e-69;
9; Mismatchcs 19; Indels 1;
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STREET: 2033 K Street, N.W., #800
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                    FILMS OAIE: 13-10N-1994
PRIOR APPLICATION NOME: 19 1994/779512
FILMS DAIR: 26-30L-1994
FILMS DAIR: 26-30L-1994
FILMS DAIR: 26-30L-1994
FERENACION HOMBER: 196-518
FERENACION HOMBER: 196-518
FERENACION HOMBER: 196-518
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01095
FILING DATE: 05-JUN-1995
                                                                                                                                                                                JP 1994/130236
                                                                                                                                                                                                                                                                                                                       DMBER: JP 1:94/173912
26-JUL-1994,
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; Patent No. 6143541
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Best Local Similarity 87.44,
Matches 202; Conservative?
                                                                                                                                       PRIOR APPLICATION DATA:
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COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 AELEGLDESPAQYMATYVMNLGIDGSGITIGIIDTGIDASHPDLQGKVIGHVDFYNGRSY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 PYDDHGHGTHVASIAAGTGAASHGXYKGMAPGAKLAGIKVLGADGSGSISTIKGVENAV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PYDDHGBGTHVASIAAGTGAASHGKYKGAAPGAKIAGIKYCAGGSGSISTIKKGVEHAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 ASKVITVGAVDSKDNIASFSSRGPTADGRLKPEVVAPGVDILAPRASGTSKGTPINDYT 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.04; Score 1918; DB 4; Length 412; Best Local Smilarity 89.54; Pred Mo C. 5.1-212; Indels C Merses 367; Conservative 13; Mismatches 28; Indels C
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APPLICARY: TSGINGSHAL
APPLICARY: ANCO, INFORMAN
APPLICARY: ANCO, INFORMAN
APPLICARY: ANCO, INFORMAN
APPLICARY: ANCO SEQUENCES
ANDRESSEE: RANDOWS:
ADDRESSEE: RANDOWS:
ADDRESSEE: RANDOWS:
ADDRESSE: A19 SWORTH STORE K M.* SILE O
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MEDICAN TIPE: Floppy disk.

COMPUTER: INA COMPETIBLE OS.

COMPUTER: INA COMPETIBLE OS.

COMPUTER: STERMING OS.

CURRANTES STERMING OS.

CURRANTES PREMIARE NEUGANOS.

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MARRIERE US/OR/750.332
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                    CORRENT FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 155959/1997
PRIOR FLILMG DATE: 1997-06-10
NUMBER OF SED ID NOS: 33
SOCHWARE: Retentin version 3.0
SEQ ID NO 1.
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Sequence 18, Application US/08750532
Patent No. 5796339
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APPLICANT: MITTA, MASSHOLI
APPLICANT: YAMAMOTO, KAISUHIKO
APPLICANT: MORISHITA, MIO
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APPLICATION NUMBER: 35/09/000,016 FILING DATE: January 30, 1998

FILING DATE: January CLASSIFICATION: 530 PRIOR APPLICATION DATA:

2355

CLASSIFICATION:

SOFTWARE: Nordperfect 5.1

Washington

20004 COUNTRY

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526 LIYRNIGTODVILKLISTATDPKGKAAPAGFPTLGATTVTVPA---GGSASVDNTADIRL 562
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TOPDLOCK: linear
MOLECULE TYPE: protein
US-09-000-016-2
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COMPUTER READABLE FORM:
MEGIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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us-09-841-553-5.rai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 LTGGKAKLSGVRFIQEDYKVTVSAELEGLOESAAQVNATYVWNLGYDGSGITIGIIOTGI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 VTNGDRTASGIAHVMLD----GVRRAALDTSVGOIGAPKAWSAGYDGKGVKTAVLDTGV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 DASHPOLOGKVIGHVOFVNGRSTPYDOHGHGTHVASIAAGTGAASNGKYXGMAPGAKLAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 INVLGADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSOAVNN-AWD 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 GKVLDDSGFGDDSGILAGMEWAA----AGGADVVNMSLGGMDTPE-TDPLEAAVDKLSAE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AGIVYCVAAGNSGPNTYTVGSPAAASKVITVGAVOSNDMIASFSSRGP-TADGRLKPEVV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     331 KGVLFAIAAGREGPE--SIGSPGSADAALTVGAVDDKDKLADFSSTGPRLGDGAIKPPVT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348 APGVDIIAPRASGTSMGTPIND---YYTKASGTSMATPHVSGVGALILOAHPSWTFPKVK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409 APGVDITAASAEGNDIGGEVGEGPAGYMTISGTSNATPHVAGAAALLKOGHPDWTSAELK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 GAL--TGSTKGGK-YTPPEGGSGRIQADKALQQTVIADPVSVSFGVOGWPHTDDEPVTKQ:525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            526 LTYRNLGTODVTLKLTSTATDPKGKAAPAGFFTLGATTVTVPA----GGSASVDXTADTRL 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNEVDYSYTAYYGFEKVGYYNPTAGIWTVKVVSY-----KGAANYOVDVVSDGS 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583 GGTVDGAYSAYVVATGGGOTVRTAAAVOREVESYDVTVRHIGRDGKPTTEHLTDLIGYAG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 LSQSGGNPNPNPNPNPNPTTTDTQTF---TGS-VNDYWDTSDTFTM-----NVNSGA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643 LGSGRGYG------APAIDIAILRLPKGTYLVDSHIAKDFGILKGGIDKLVQPKLSV 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               586 TKITGDLTFOT-SYNDLDLYLYDPNGNLVDRSTSSNSYEHVBYANPAPGTHTFLYYAYST 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: HOTSON N. Check, Jr. REJESPRACHON NUMBER: 33.367 REPERVECTOR NUMBER: TELECOMMUNICATION INCORAFION: TELEPHONE: 202-721-8200 TELEFAX: 102-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Sequence 2, Application US/09000016
; Patent ND. 6143541
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEG ID HD: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 734 amino acids
TYPE: amino acid
STRANEENESS: single
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 TOPOLOGY: linear
7 MOLECULE TYPE: protein
US-09-000-016-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           645 YG 646
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10,2%; Score 692.5; DB 4; Length 823;
BBSE Local Similarity 91,6%; Pred, No. 2.3e-4.2;
GARCHES 202, Conservative 62; Mismatches 223; Indels 115; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 LTGGKAKLSGVRFLQEDYR/TVSARLEGLDESAAQVMATYVWNLGYDGSGITIGIIDTGI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 VTNGDRTASGIAHVMLD-----GVRRAALOTSVGQIGAPKAMSAGYDGKGVKIAVLDTGV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 DASHPDLQGKVIGWVQPTNGRSYPYDDHGHGPHVASIAAG7GAASNGKYKGMAPGAKLAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 DTSHPDLKGRVTASKMPTAAPG-AGDKVGHGTHVASIAAGTGAQSKGKYKGVAPGAAILN 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 IKVLGADGSGSISTIIK(:VEMAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNN-AWD 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 GKYLODSGFGDOSGILAGMEWAA----AQSADVVNMSLGGMD7PE-TDPLEAAVOKLSAE 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 KGVLFAIAAGNEGPE--11GSPGSADAALTVGAVDDKDKLADPSSTGPRLGDGAIKPDVT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 APGVOLIAPRASGTSMGTPIND -- - YYTKASGTSMATPHVSGVGALILQAHPSWTPOKVK 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            469 GAL--TGSTKGGK-YTPFELD/SGRIQADKALQQTVIADPVSVSFGVQQWPHTDDEPVTKQ 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              437 -----YDDYAKLTP7GSYADKGSATHTFDVSGATFVTATLYHDTGSSDIDLYLYDPN 468
                                                                                                                                                                                                                                                                                                             NOORESEE: Nenderoit, Lind & Ponack, L.L.P.
STREET: 2033 K Street, M.H., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/O9/000,016
FILING DATE: January 39, 1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 18M COMPALIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: Wordparfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEOURNE CHRACTERISTICS: LEWOTH: 823 mmino acide TYPE: amino acid
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60 GHGTHVASIAAGTCAQSKGKYKGVAPGAAILNGKVLDDSGFGDDSGILAGMENRA----A 115
                                          258 YGIKYINLSLGSSQSSDGTGSLSOAVNN-AMDAGIVVCVAAGNSGPNTYTVGSPAAASKV 316
                                                                  317 ITVGAVDSNDNIASFSSRGP-7ADGRLKPEVVAPGVDIIAPRASGTSMGTPIND---YYT 372
                                                                                                                                                                                                                      373 KASGTSMATPHVSGVGALILQAHPSWTPDKVKTALIETADIVAPKEIADIAYGAGRVNVY 432
                                                                                                                                                                                                                                                                                                            433 KAIK-----YDDYAKLTFTGSVADKGSAT 456
                                                                                                                                                                                                                                                                                                                                                  290 KALQOTVIADPVSVSFGVQQMPHTDDEPVTKQLTYRNLGTQDVTLKLTSTATDPXGKAAP 349
                                                                                                                                                                                                                                                                                                                                                                                             457 HTEDVSGATEVIALLYHOLGSSOIDLILYDPNGNEVDYSYTAYYGFEKUGYYNPTAGTWI 516
                                                                                                                                                                                                                                                                                                                                                                                                                                             350 AGPFILGAITVTVDA---UGSA3VDNTADTRLGGTVDGAYSAYVVATGGGUTVRTAAAVO 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   517 VKVVSY-----KGAANYQVDVVSDGSLSQSGGNPNPNPNPNPTPTTDTQTF-- 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         407 REVESYDVTVRHIGRDGKPTTEHL/DLIGYAGLGSGRGYG------APATD/ATLRL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hile: ETLS STORY BACILLUS LICHENIFORMIS TITLE OF INVENTION: PND-1 KERATINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTHARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US.08/250,028
FILING DATE: 27-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/685,774
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSER: Kenneth D. Sibley
STREET: Post Office Drayer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/UR685774
Patent No. 5712147
GENERAL INFORMATION:
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No. 5712147th Carolina
Y: USA
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CONPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/NS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sibley, Kenneth D. REGISTRATION NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shih, Jason C. H. APPLICANT: Lin, Xiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 -TGS-VNDWWDTSDTFTH 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 PKGTYLVDSWIAKDFGTL 475
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KNFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 379 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES
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STATE: No.
COUNTRY: USA
28234
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US-08-685-774-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 GHCTHVASIAAGTGAASHGKYKGMAPQAKLAGIKVLGADGSGSISTIIKGVEMAVDNKDK 25761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LDTSVQQIGAPKAMSAQYDGKGVKIAVLDTGVDTSHPDLKGRVTASKNPTAAPG-AG/XV, 59
                                          583 GGTVDGAYSAYVVATGGGGTVRTAAAVQREVESYDVTVRHIGRDGKPTTEHLTDLIGYAG 642
                                                                                                                  643 LGSGRQYG------APARDTATLRLPKGTYLVDSWIAKDFGTLKGGIDWLVQPKLSV 693
    489 GNEVDYSYTAYYGFEKVGYYNDTAGTWTVKVVSY-----KGAANYQVDVVSDGS 537
                                                                                          538 LSOSCOGNPNPNPNPNPNPTPTTDTQTF---TGS-VNDYNDTSDTFTM-----NVNSGA 585
                                                                                                                                                                           586 TKITGDLIFDT-SYNDLDLYLYDPNGNLVDRSTSSNSYEHVZYANPAPGTWIFLVYAYST 644
                                                                                                                                                                                                                      694 TKDT-TLTLDARITKAADITVPDPK------AKPLSAT--ICYTYDI 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.8%; Score 679.5; DB 4: Length 520; 36.3%; Pred. No. 1.1e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESS:
STREET: 2013 K Street, N.W., #800
CIT: Weathington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
HEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible COMPATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             January 30, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09000016
Patent No. 6183541
GENERAL INFORMATION:
APPLICANT: AKITA ARISAMA et el.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warren W. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/
FILING DATE: January 30, 1
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SEQUENCE CHARACTERISTICS:
LENGTH: 520 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
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US-09-000-016-7
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20006
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US-09-000-016-7
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ORIGINAL SOURCE: ORGANISM: Bac -GMA

US-D8-685-774-2

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251 ASGVIVVAAAGNEGISGSSTVGYPGYPGYPSVIAVGAVDSSNQRASPSSVGPELD----- 304
                                                                                                                                                                                                                57 ERISTVIVPENHREKEIAVR---VLRLMGAKVRYVYHIIPAIAADLK---VRDLLVISGL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 TGGKAKLSGVRFIQEDYKVTVSAELEGLDESAAOVMATYVWNLGYDGSGITIGIIDYGID 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 ----KKDPSVAYVEEDH--VAHAYAQSVPYGVSQIKAPALHSQGYTGSNVKVAVIDSGID 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 AGIXVIGADGSGSISTIIKGVEWAVDNKDKYGIKVINLSLGSSQSSDGTDSLSQAVNNAW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 YAVKVICADGSQQYSWIINGIEWALAN----NMDVINMSLG---GPSGSAALKAAVDKAV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 DAGIVNCVAAGNSGP--NTYTVGSPAAASKVITVGAVDSNDNIASFSSRGPTADGRLKPE 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 VVAPGVDILAPRASGISMCIFINDYYTKASGISMATPHVSGVGALILQAHPSW7PDKVK7 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 -----INGEKOTMSTNEAARKEDVISEKGGKVOKOFKYVDAASATLHEKAVKEL----- 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seemin () 197343
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CURRENT APPLICATION KINNER: SUSSTITUTION KINNER: SUSSTITUTION (* 1951) 09
FLING DATE: 1991) 09
ATTORNEY/AGENT INFORMATION
NAME: BERT SCHEMENTON: REGISTRATION WINNER: SUSSTITUTION (* 1951)
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COUNTRY: USA
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US-07-772-087-4
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16.24: Score 557; DB 1; Length 379;
See Local Similarity 3.0, Pred; No. 5.79-31 Indels 74; Gapp
Motches 153; Conservative 62; Mismatches 188; Indels 74; Gapp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 YVERDH--VAHALAQTVPYGIPLIKADKVQAQGPKGANYKVAVLDTGIQASHPDL--NVV 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GLKALILVILVLGLYVGSVAAAPEKKVEQVRHVEKHYGLLTPGLFRKIGKLNPNEEISTV 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 VGPKSGVKTASVKKDVIKESGGKVDKQPRIINAAKAKLDKEALKEVK-----HDPDVA 94
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35.1%; Pred. No. 8.1e-33;
14e 65; Mismatches 141; Indels 86;
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RESULT 14 509-445-472-31 5 Sequence 31. Application US/09445472 : Patent No. 6358726

ORGANISM: Bacillus subtilis 35-09-445-472-31

Best Local Similarity 35.1% Matches 158; Conservative

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uery Match

418 EIADIAYGAGRVNVYKA 434

900

363 -- SSPYYGKGLINVEAA 377

us-09-841-553-5.rai

3 GERALILVILVIGLYVGSVAAAPERKVEQVRAVERNYGLLTPGLPRKIGKLNPNEKISTV 63 54; Mismatches 150; Indels 73; Query Match 16.2%; Score 554.5; 09 1; Length 379; Best Local S;milarity 34.2% Pred No. 676-279; Greet Local State 64; Mismatches 150; Indels 73; Mismatches 150; Locals 73; Mismatches 150; Mismatches 150; Locals 73; Mismatches 150; Mismat ò

183 WVDFVNGRSYPYDDHGHGTHVASIAAGTGAASNGK--YKGNAPGAKLAGIKVLGADGSGS 240 95 VEEDH--VAHALAGTVPYGIPLIKADKVQAQGFKGANVKVAVLDTGIQASHPDL--NVVG

151 GASFVAGEAYNTDGNGHGTHV----AGTVAALDNTTGVLGVAFSVSLYAVKVLNSSGSGT

Search completed: October 31, 2002, 13:31:28 Job time : 15 secs

362 -SSPYYGKGLINVEAA 376